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| | |
|----------------|---|
| NEWS 1 | Web Page for STN Seminar Schedule - N. America |
| NEWS 2 APR 04 | STN AnaVist, Version 1, to be discontinued |
| NEWS 3 APR 15 | WPIDS, WPINDEX, and WPIX enhanced with new predefined hit display formats |
| NEWS 4 APR 28 | EMBASE Controlled Term thesaurus enhanced |
| NEWS 5 APR 28 | IMSRESEARCH reloaded with enhancements |
| NEWS 6 MAY 30 | INPAFAMDB now available on STN for patent family searching |
| NEWS 7 MAY 30 | DGENE, PCTGEN, and USGENE enhanced with new homology sequence search option |
| NEWS 8 JUN 06 | EPFULL enhanced with 260,000 English abstracts |
| NEWS 9 JUN 06 | KOREPAT updated with 41,000 documents |
| NEWS 10 JUN 13 | USPATFULL and USPAT2 updated with 11-character patent numbers for U.S. applications |
| NEWS 11 JUN 19 | CAS REGISTRY includes selected substances from web-based collections |
| NEWS 12 JUN 25 | CA/Caplus and USPAT databases updated with IPC reclassification data |
| NEWS 13 JUN 30 | AEROSPACE enhanced with more than 1 million U.S. patent records |
| NEWS 14 JUN 30 | EMBASE, EMBAL, and LEMBASE updated with additional options to display authors and affiliated organizations |
| NEWS 15 JUN 30 | STN on the Web enhanced with new STN AnaVist Assistant and BLAST plug-in |
| NEWS 16 JUN 30 | STN AnaVist enhanced with database content from EPFULL |
| NEWS 17 JUL 28 | CA/Caplus patent coverage enhanced |
| NEWS 18 JUL 28 | EPFULL enhanced with additional legal status information from the epoline Register |
| NEWS 19 JUL 28 | IFICDB, IFIPAT, and IFIUDB reloaded with enhancements |
| NEWS 20 JUL 28 | STN Viewer performance improved |
| NEWS 21 AUG 01 | INPADOCDB and INPAFAMDB coverage enhanced |
| NEWS 22 AUG 13 | CA/Caplus enhanced with printed Chemical Abstracts page images from 1967-1998 |
| NEWS 23 AUG 15 | CAOLD to be discontinued on December 31, 2008 |
| NEWS 24 AUG 15 | Caplus currency for Korean patents enhanced |
| NEWS 25 AUG 25 | CA/Caplus, CASREACT, and IFI and USPAT databases enhanced for more flexible patent number searching |
| NEWS 26 AUG 27 | CAS definition of basic patents expanded to ensure comprehensive access to substance and sequence information |
| NEWS 27 SEP 18 | Support for STN Express, Versions 6.01 and earlier, to be discontinued |
| NEWS 28 SEP 25 | CA/Caplus current-awareness alert options enhanced to accommodate supplemental CAS indexing of exemplified prophetic substances |

NEWS 29 SEP 26 WPIDS, WPINDEX, and WPIX coverage of Chinese and Korean patents enhanced
NEWS 30 SEP 29 IFICLs enhanced with new super search field
NEWS 31 SEP 29 EMBASE and EMBAL enhanced with new search and display fields
NEWS 32 SEP 30 CAS patent coverage enhanced to include exemplified prophetic substances identified in new Japanese-language patents

NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,
AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.

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NEWS IPC8 For general information regarding STN implementation of IPC 8

Enter NEWS followed by the item number or name to see news on that specific topic.

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FILE 'HOME' ENTERED AT 04:02:48 ON 01 OCT 2008

=> index bioscience
FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED
COST IN U.S. DOLLARS

FULL ESTIMATED COST

INDEX 'ADISICTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 04:03:14 ON 01 OCT 2008

69 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view search error messages that display as 0* with SET DETAIL OFF.

=> s biofilm and remov?(p)biofilm and protease and esterase and amylase and solut? and alkaline and wash?

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0* FILE ADISNEWS  
0* FILE ANTE  
0* FILE AQUALINE  
0* FILE BIOENG  
0* FILE BIOTECHABS  
0* FILE BIOTECHDS  
0* FILE BIOTECHNO  
0* FILE CEABA-VTB  
0* FILE CIN  
0* FILE ESBIOBASE
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30 FILES SEARCHED...
0* FILE FOMAD
0* FILE FOREGE
0* FILE FROSTI
0* FILE FSTA

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1   FILE GENBANK
1   FILE IFIPAT
0*  FILE KOSMET
0*  FILE NTIS
0*  FILE NUTRACEUT
0*  FILE PASCAL
0*  FILE PHARMAML
60 FILES SEARCHED...
11   FILE USPATFULL
4    FILE USPAT2
0*  FILE WATER
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4 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STNINDEX

L1 QUE BIOFILM AND REMOV?(P) BIOFILM AND PROTEASE AND ESTERASE AND AMYLASE AND SOLUT? AND ALKALINE AND WASH?

=> file genbank ifipat uspatfull uspat2
COST IN U.S. DOLLARS SINCE FILE TOTAL
FULL ESTIMATED COST ENTRY SESSION
 2.60 2.81

FILE 'GENBANK' ENTERED AT 04:05:30 ON 01 OCT 2008

FILE 'IFIPAT' ENTERED AT 04:05:30 ON 01 OCT 2008
COPYRIGHT (C) 2008 IFI CLAIMS(R) Patent Services (IFI)

FILE 'USPATFULL' ENTERED AT 04:05:30 ON 01 OCT 2008
CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'USPAT2' ENTERED AT 04:05:30 ON 01 OCT 2008
CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

=> s 11
L2 17 L1

=> dup rem 12
DUPLICATE IS NOT AVAILABLE IN 'GENBANK'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L2
L3 13 DUP REM L2 (4 DUPLICATES REMOVED)

=> d 13 1-13

L3 ANSWER 1 OF 13 USPATFULL on STN
AN 2008:29739 USPATFULL
TI Removable antimicrobial coating compositions and methods of use
IN Lu, Helen S.M., Wallingford, PA, UNITED STATES
 Hoffmann, Christian, Newark, DE, UNITED STATES
 Lenges, Christian Peter, Wilmington, DE, UNITED STATES
 Stieglitz, Barry, Wynnewood, PA, UNITED STATES
 Leger, Lynn, Mississauga, CANADA
 VanGorp, Judith Johanna, Wilmington, DE, UNITED STATES
 Malone, Shaun F., Ajax, CANADA
PI US 20080026026 A1 20080131
AI US 2007-710290 A1 20070223 (11)
PRAI US 2006-776081P 20060223 (60)
 US 2006-831983P 20060719 (60)
DT Utility
FS APPLICATION
LN.CNT 2260
INCL INCLM: 424/405.000

INCLS: 422/028.000
NCL
NCLM: 424/405.000
NCLS: 422/028.000
IC IPCI A01N0025-00 [I,A]; A01P0001-00 [I,A]; A61L0002-00 [I,A]
IPCR A01N0025-00 [I,C]; A01N0025-00 [I,A]; A01P0001-00 [I,C];
A01P0001-00 [I,A]; A61L0002-00 [I,C]; A61L0002-00 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 2 OF 13 USPATFULL on STN
AN 2007:314900 USPATFULL
TI Removable antimicrobial coating compositions and methods of use
IN Lu, Helen S.M., Wallingford, PA, UNITED STATES
Hoffmann, Christian, Newark, DE, UNITED STATES
Lenges, Christian Peter, Wilmington, DE, UNITED STATES
Leger, Lynn, Mississauga, CANADA
Malone, Shaun F., Ajax, CANADA
Stieglitz, Barry, Wynnewood, PA, UNITED STATES
Van Gorp, Judith Johanna, Wilmington, DE, UNITED STATES
PI US 20070275101 A1 20071129
AI US 2007-710325 A1 20070223 (11)
PRAI US 2006-776081P 20060223 (60)
US 2006-831983P 20060719 (60)
DT Utility
FS APPLICATION
LN.CNT 2259
INCL INCLM: 424/719.000
INCLS: 106/015.050; 514/642.000
NCL NCLM: 424/719.000
NCLS: 106/015.050; 514/642.000
IC IPCI A01N0033-12 [I,A]; A01N0033-00 [I,C*]; A01P0001-00 [I,A];
A01P0013-00 [I,A]; A01P0003-00 [I,A]
IPCR A01N0033-00 [I,C]; A01N0033-12 [I,A]; A01P0001-00 [I,C];
A01P0001-00 [I,A]; A01P0003-00 [I,C]; A01P0003-00 [I,A];
A01P0013-00 [I,C]; A01P0013-00 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 3 OF 13 IFIPAT COPYRIGHT 2008 IFI on STN
AN 10840879 IFIPAT;IFIIDB;IFICDB
TI Method of removing a biofilm; Washing
simultaneously or consecutively in solution comprising an
enzyme mixture containing at least one protease, at least one
esterase, and an amylase in a detergent with an
alkaline pH
IN Marion Karine
PA Unassigned Or Assigned To Individual (68000)
PPA karine Marion thierry Sanchez (Probable)
PI US 20050079594 A1 20050414
AI US 2003-695823 20031030
PRAI FR 2002-13963 20021031
US 2002-422508P 20021031 (Provisional)
FI US 20050079594 20050414
DT Utility; Patent Application - First Publication
FS CHEMICAL
APPLICATION
ED Entered STN: 19 Apr 2005
Last Updated on STN: 23 Aug 2007
CLMN 22

L3 ANSWER 4 OF 13 USPATFULL on STN
AN 2005:208966 USPATFULL
TI Protein variants having modified immunogenicity
IN Roggen, Erwin Ludo, Lyngby, DENMARK

Ernst, Steffen, Broenshoej, DENMARK
Svendsen, Allan, Hoersholm, DENMARK
Friis, Esben Peter, Valby, DENMARK
Osten, Claus Von Der, Lyngby, DENMARK

PA Novozymes A/S, Bagsvaerd, DENMARK (non-U.S. corporation)
PI US 20050181446 A1 20050818
AI US 2001-957806 A1 20010921 (9)
PRAI WO 2001-DK293 20010430
DK 2000-707 20000428
DK 2001-327 20010228
US 2000-203345P 20000510 (60)
US 2001-277817P 20010321 (60)

DT Utility
FS APPLICATION
LN.CNT 12950
INCL INCLM: 435/007.100
INCLS: 435/069.100; 435/320.100; 435/325.000; 702/019.000; 435/005.000
NCL NCLM: 435/007.100
NCLS: 435/005.000; 435/069.100; 435/226.000; 435/320.100; 435/325.000;
506/014.000; 530/350.000; 702/019.000

IC [7]
ICM C12Q001-70
ICS G01N033-53; G06F019-00; G01N033-48; G01N033-50; C12P021-02;
C12N005-06
IPCI C12Q0001-70 [ICM,7]; G01N0033-53 [ICS,7]; G06F0019-00 [ICS,7];
G01N0033-48 [ICS,7]; G01N0033-50 [ICS,7]; C12P0021-02 [ICS,7];
C12N0005-06 [ICS,7]
IPCR A21D0002-00 [I,C*]; A21D0002-26 [I,A]; A21D0008-02 [I,C*];
A21D0008-04 [I,A]; C07K0001-00 [I,C*]; C07K0001-04 [I,A];
C07K0005-00 [I,C*]; C07K0005-103 [I,A]; C07K0005-11 [I,A];
C07K0005-113 [I,A]; C07K0016-40 [I,C*]; C07K0016-40 [I,A];
C11D0003-38 [I,C*]; C11D0003-386 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 5 OF 13 USPATFULL on STN
AN 2005:104955 USPATFULL
TI Multimolecular devices and drug delivery systems
IN Cubicciotti, Roger S., Montclair, NJ, UNITED STATES
PI US 20050089890 A1 20050428
AI US 2004-872973 A1 20040621 (10)
RLI Division of Ser. No. US 2001-907385, filed on 17 Jul 2001, GRANTED, Pat.
No. US 6762025 Continuation of Ser. No. US 1998-81930, filed on 20 May
1998, GRANTED, Pat. No. US 6287765

DT Utility
FS APPLICATION
LN.CNT 15620
INCL INCLM: 435/006.000
INCLS: 530/395.000
NCL NCLM: 435/006.000
NCLS: 530/395.000
IC [7]
ICM C12Q001-68
ICS C07K014-00
IPCI C12Q0001-68 [ICM,7]; C07K0014-00 [ICS,7]
IPCR C07H0021-00 [I,C*]; C07H0021-00 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 6 OF 13 USPATFULL on STN DUPLICATE 1
AN 2004:144188 USPATFULL
TI METHODS FOR ELIMINATING THE FORMATION OF BIOFILM
IN Xu, Feng, Davis, CA, UNITED STATES
PA Novozymes Biotech, Inc., Davis, CA, UNITED STATES, 95616 (U.S.)

corporation)
PI US 20040109852 A1 20040610
US 6777223 B2 20040817
AI US 2001-885379 A1 20010619 (9)
RLI Continuation-in-part of Ser. No. US 2000-596795, filed on 19 Jun 2000,
ABANDONED
DT Utility
FS APPLICATION
LN.CNT 995
INCL INCLM: 424/094.600
INCLS: 424/094.200
NCL NCLM: 435/262.500; 424/094.600
NCLS: 210/632.000; 424/094.100; 424/094.200; 435/189.000; 435/190.000
IC [7]
 ICM A61K038-54
 ICS A61K038-46
 IPCI A61K038-54 [ICM,7]; A61K038-46 [ICS,7]; A61K038-43 [ICS,7,C*]
 IPCI-2 C12S0009-00 [ICM,7]; A61K038-43 [ICS,7]
 IPCR A61L0002-18 [I,C*]; A61L0002-18 [I,A]; B08B0007-00 [I,C*];
 B08B0007-00 [I,A]; C02F0001-50 [I,C*]; C02F0001-50 [I,A];
 C12S0009-00 [I,C*]; C12S0009-00 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 7 OF 13 USPATFULL on STN DUPLICATE 2
AN 2003:37665 USPATFULL
TI Polypeptides having lactonohydrolase activity and nucleic acids encoding
same
IN Berka, Randy M., Davis, CA, UNITED STATES
Rey, Michael W., Davis, CA, UNITED STATES
PA Novozymes Biotech, Inc., Davis, CA, UNITED STATES, 95616 (U.S.
corporation)
PI US 20030027310 A1 20030206
US 6756220 B2 20040629
AI US 2002-126170 A1 20020419 (10)
RLI Division of Ser. No. US 1999-434690, filed on 5 Nov 1999, GRANTED, Pat.
No. US 6395529 Continuation-in-part of Ser. No. US 1999-263041, filed on
5 Mar 1999, ABANDONED Continuation-in-part of Ser. No. US 1998-189497,
filed on 10 Nov 1998, ABANDONED
DT Utility
FS APPLICATION
LN.CNT 2289
INCL INCLM: 435/196.000
INCLS: 435/069.100; 435/320.100; 435/325.000; 536/023.200
NCL NCLM: 435/197.000; 435/196.000
NCLS: 435/252.300; 435/320.100; 435/929.000; 530/350.000; 536/023.200;
 435/069.100; 435/325.000
IC [7]
 ICM C12N009-16
 ICS C07H021-04; C12P021-02; C12N005-06
 IPCI C12N0009-16 [ICM,7]; C07H021-04 [ICS,7]; C07H021-00 [ICS,7,C*];
 C12P021-02 [ICS,7]; C12N0005-06 [ICS,7]
 IPCI-2 C12N0009-16 [ICM,7]; C12N0001-20 [ICS,7]; C12N0015-00 [ICS,7];
 C07H021-04 [ICS,7]; C07H021-00 [ICS,7,C*]
 IPCR C02F0001-50 [I,C*]; C02F0001-50 [I,A]; C12N0009-18 [I,C*];
 C12N0009-18 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 8 OF 13 USPATFULL on STN DUPLICATE 3
AN 2002:148647 USPATFULL
TI 2,6-beta-D-fructan hydrolase enzyme and processes for using the enzyme
IN Moller, Soren, Holte, DENMARK
Johansen, Charlotte, Holte, DENMARK

Schafer, Thomas, Farum, DENMARK
Ostergaard, Peter Rahbek, Virum, DENMARK
Hoeck, Lisbeth Hedegaard, Skodsborg, DENMARK
PA Novozymes A/S, Bagsvaerd, DENMARK, DK-2880 (non-U.S. corporation)
PI US 20020076790 AI 20020620
US 6524827 B2 20030225
AI US 2001-969362 AI 20011002 (9)
RLI Division of Ser. No. US 1999-397885, filed on 17 Sep 1999, GRANTED, Pat. No. US 6323007
PRAI DK 1998-1173 19980918
DK 1998-1623 19981209
US 1998-101615P 19980924 (60)
US 1998-111675P 19981210 (60)
DT Utility
FS APPLICATION
LN.CNT 3312
INCL INCLM: 435/200.000
INCLS: 435/069.100; 435/325.000; 435/320.100; 435/101.000; 536/023.200
NCL NCLM: 435/074.000; 435/200.000
NCLS: 435/183.000; 435/252.300; 435/252.330; 435/320.100; 536/023.200;
435/069.100; 435/101.000; 435/325.000
IC [7]
ICM C12P019-44
ICS C07H021-04; C12N009-24; C12P021-02; C12N005-06
IPCI C12P0019-44 [ICM,7]; C12P0019-00 [ICM,7,C*]; C07H0021-04 [ICS,7];
C07H0021-00 [ICS,7,C*]; C12N0009-24 [ICS,7]; C12P0021-02 [ICS,7];
C12N0005-06 [ICS,7]
IPCI-2 C12N0009-24 [ICM,7]
IPCR A61K0008-30 [I,C*]; A61K0008-64 [I,A]; A61K0008-66 [I,A];
A61Q0011-00 [I,C*]; A61Q0011-00 [I,A]; A61Q0017-00 [I,C*];
A61Q0017-00 [I,A]; C11D0003-38 [I,C*]; C11D0003-386 [I,A];
C12N0009-24 [I,C*]; C12N0009-24 [I,A]; C12P0019-00 [I,C*];
C12P0019-14 [I,A]; C12P0019-44 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 9 OF 13 USPATFULL on STN DUPLICATE 4
AN 2002:60923 USPATFULL
TI Single-molecule selection methods and compositions therefrom
IN Cubicciotti, Roger S., Montclair, NJ, UNITED STATES
PI US 20020034757 AI 20020321
US 6762025 B2 20040713
AI US 2001-907385 AI 20010717 (9)
RLI Continuation of Ser. No. US 1998-81930, filed on 20 May 1998, GRANTED,
Pat. No. US 6287765
DT Utility
FS APPLICATION
LN.CNT 15716
INCL INCLM: 435/006.000
INCLS: 435/091.200; 536/022.100; 536/023.100; 536/024.300
NCL NCLM: 435/006.000
NCLS: 435/091.200; 536/022.100; 536/023.100; 536/024.300; 536/024.500
IC [7]
ICM C12Q001-68
ICS C07H019-00; C07H021-00; C07H021-02; C07H021-04; C12P019-34
IPCI C12Q0001-68 [ICM,7]; C07H0019-00 [ICS,7]; C07H0021-00 [ICS,7];
C07H0021-02 [ICS,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
C12P0019-34 [ICS,7]; C12P0019-00 [ICS,7,C*]
IPCI-2 C12Q0001-68 [ICM,7]; C12P0019-34 [ICS,7]; C12P0019-00 [ICS,7,C*];
C07H0021-02 [ICS,7]; C07H0021-00 [ICS,7,C*]
IPCR C07H0021-00 [I,C*]; C07H0021-00 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 10 OF 13 USPATFULL on STN
AN 2002:122473 USPATFULL
TI Polypeptides having lactonohydrolase activity and nucleic acids encoding same
IN Berka, Randy M., Davis, CA, United States
Rey, Michael W., Davis, CA, United States
PA Novozymes Biotech, Inc., Davis, CA, United States (U.S. corporation)
PI US 6395529 B1 20020528
AI US 1999-434690 19991105 (9)
RLI Continuation-in-part of Ser. No. US 1999-263041, filed on 5 Mar 1999,
now abandoned Continuation-in-part of Ser. No. US 1998-189497, filed on
10 Nov 1998, now abandoned
DT Utility
FS GRANTED
LN.CNT 2055
INCL INCLM: 435/197.000
INCLS: 435/252.300; 435/320.100; 435/929.000; 536/023.200; 530/350.000
NCL NCLM: 435/197.000
NCLS: 435/252.300; 435/320.100; 435/929.000; 530/350.000; 536/023.200
IC [7]
ICM C12N009-16
ICS C12N001-20; C12N015-00; C12N001-00; C07H021-04
IPCI C12N009-16 [ICM,7]; C12N001-20 [ICS,7]; C12N0015-00 [ICS,7];
C12N001-00 [ICS,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*]
IPCR C02F0001-50 [I,C*]; C02F0001-50 [I,A]; C12N0009-18 [I,C*];
C12N0009-18 [I,A]
EXF 435/197; 435/252.3; 435/320.1; 435/929; 536/23.2; 530/350
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 11 OF 13 USPATFULL on STN
AN 2001:214863 USPATFULL
TI 2,6- β -D-fructan hydrolase enzyme and processes for using the enzyme
IN Moller, Soren, Holte, Denmark
Johansen, Charlotte, Holte, Denmark
Schafer, Thomas, Farum, Denmark
Ostergaard, Peter Rahbek, Virum, Denmark
Hoeck, Lisbeth Hedegaard, Skodsborg, Denmark
PA Novozymes A/S, Bagsvaerd, Denmark (non-U.S. corporation)
PI US 6323007 B1 20011127
AI US 1999-397885 19990917 (9)
PRAI DK 1998-1173 19980918
DK 1998-1623 19981209
US 1998-101615P 19980924 (60)
US 1998-111675P 19981210 (60)
DT Utility
FS GRANTED
LN.CNT 2422
INCL INCLM: 435/074.000
INCLS: 435/200.000; 435/252.330; 435/262.000; 435/274.000; 435/320.100
NCL NCLM: 435/074.000
NCLS: 435/200.000; 435/252.330; 435/262.000; 435/274.000; 435/320.100
IC [7]
ICM C12P019-44
IPCI C12P0019-44 [ICM,7]; C12P0019-00 [ICM,7,C*]
IPCR A61K0008-30 [I,C*]; A61K0008-64 [I,A]; A61K0008-66 [I,A];
A61Q0011-00 [I,C*]; A61Q0011-00 [I,A]; A61Q0017-00 [I,C*];
A61Q0017-00 [I,A]; C11D0003-38 [I,C*]; C11D0003-386 [I,A];
C12N0009-24 [I,C*]; C12N0009-24 [I,A]; C12P0019-00 [I,C*];
C12P0019-14 [I,A]; C12P0019-44 [I,A]
EXF 536/23.1; 530/350; 435/183; 435/74; 435/200; 435/252.33; 435/262;
435/274; 435/320.1
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 12 OF 13 USPATFULL on STN
AN 2001:152673 USPATFULL
TI Methods for detecting and identifying single molecules
IN Cubicciotti, Roger S., Montclair, NJ, United States
PA Molecular Machines, Inc., Montclair, NJ, United States (U.S.
corporation)
PI US 6287765 B1 20010911
AI US 1998-81930 19980520 (9)
DT Utility
FS GRANTED
LN.CNT 15456
INCL INCLM: 435/006.000
INCLS: 435/091.200; 536/022.100; 536/023.100; 536/024.300; 536/024.500
NCL NCLM: 435/006.000
NCLS: 435/091.200; 536/022.100; 536/023.100; 536/024.300; 536/024.500;
977/853.000
IC [7]
ICM C12Q001-08
ICS C12P019-34; C07M021-02
IPCI C12Q0001-08 [ICM,7]; C12Q0001-06 [ICM,7,C*]; C12P0019-34 [ICS,7];
C12P0019-00 [ICS,7,C*]; C07M0021-02 [ICS,7]
IPCR C07H0021-00 [I,A]; C07H0021-00 [I,C*]
EXF 435/6; 435/91.2; 536/22.1; 536/23.1; 536/24.3; 536/24.5
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 13 OF 13 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): AE009952 GenBank (R)
GenBank ACC. NO. (GBN): AE009952 AE013601-AE014015
GenBank VERSION (VER): AE009952.1 GI:22002119
SEQUENCE LENGTH (SQL): 4600755
MOLECULE TYPE (CI): DNA; circular
DIVISION CODE (CI): Bacteria
DATE (DATE): 2 May 2006
DEFINITION (DEF): Yersinia pestis KIM, complete genome.
SOURCE: Yersinia pestis KIM
ORGANISM (ORGN): Yersinia pestis KIM
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriales; Enterobacteriaceae; Yersinia

COMMENT:

On or before May 2, 2006 this sequence version replaced
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 REFERENCE:
 AUTHOR (AU): Deng,W.; Burland,V.; Plunkett,G. III; Boutin,A.;
 Mayhew,G.F.; Liss,P.; Perna,N.T.; Rose,D.J.; Mau,B.;
 Zhou,S.; Schwartz,D.C.; Fetherston,J.D.; Lindler,L.E.;
 Brubaker,R.R.; Plana,G.V.; Straley,S.C.;
 McDonough,K.A.; Nilles,M.L.; Matson,J.S.;
 Blattner,F.R.; Perry,R.D.
 TITLE (TI): Genome Sequence of *Yersinia pestis* KIM
 JOURNAL (SO): J. Bacteriol., 184 (16), 4601-4611 (2002)
 OTHER SOURCE (OS): CA 137:120475
 REFERENCE:
 AUTHOR (AU): Deng,W.; Burland,V.; Plunkett,G. III; Boutin,A.;
 Mayhew,G.F.; Liss,P.; Perna,N.T.; Rose,D.J.; Mau,B.;
 Zhou,S.; Schwartz,D.C.; Fetherston,J.D.; Lindler,L.E.;
 Brubaker,R.R.; Plana,G.V.; Straley,S.C.;
 McDonough,K.A.; Nilles,M.L.; Matson,J.S.;
 Blattner,F.R.; Perry,R.D.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (21-FEB-2002) Genetics, University of
 Wisconsin, 445 Henry Mall, Madison, WI 53706, USA

| FEATURES (FEAT): | | | |
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/mol-type="genomic DNA"
/strain="KIM"
/db-xref="taxon:187410" | |
| gene | complement(21..461) | /gene="mioC"
/locus-tag="y0001" | |
| CDS | complement(21..461) | /gene="mioC"
/locus-tag="y0001"
/function="factor; DNA -
replication, repair,
restriction/modification"
/note="residues 1 to 146 of 146
are 67.12 pct identical to
residues 1 to 146 of 147 from E.
coli K12 : B3742; residues 1 to
146 of 146 are 68.49 pct identical
to residues 1 to 146 of 147 from
GenPept : >gb AAL22733.1
(AE008881) initiation of
chromosome replication [Salmonella
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/note="residues 3 to 153 of 153 are 84.76 pct identical to residues 2 to 152 of 152 from E. coli K12 : B3743; residues 3 to 153 of 153 are 86.09 pct identical to residues 2 to 152 of 152 from GenPept : >emb CAD03119.1 (AL627280) regulatory protein (Salmonella enterica subsp. enterica serovar Typhi)"
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/translation="MSEIYQIDNLDRSILKALME NARTPYAELAKNLA VSPGTIHVRV EKMRQAGII TAA CVHVNPKQLGYDVCCFIGIILK SAKD YPSALKKLES LEEVVEAYYT TGHYSIFIKVMCKSIS DALQQVLINKIQTIDEIQS TETLISLQNPI MRTIVP"
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/locus-tag="y0003" |
| CDS | 1185..2177 | /gene="asnA"
/locus-tag="y0003"
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/locus-tag="y0004"
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| gene | complement (2276..3742) | /note="residues 57 to 488 of 488 are 65.04 pct identical to residues 1 to 427 of 427 from E. coli K12 : B3745; residues 1 to 488 of 488 are 64.34 pct identical to residues 1 to 483 of 483 from GenPept : >dbj BAB38110.1 (AP002566) hypothetical protein [Escherichia coli O157:H7]"
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HLQRGDYQLLQYGFDFLQQQPELI
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RWKR" |
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/note="residues 1 to 496 of 517
are 67.54 pct identical to
residues 9 to 504 of 506 from E.
coli K12 : B3746"
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regulator"
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RQPSTLSLPGATTTSVPPELLLAL
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FQQQKHSGH" |
| gene | 5573..7441 | /gene="kup"
/locus-tag="y0006"
/gene="kup"
/locus-tag="y0006"
/function="transport; transport of
small molecules; cations"
/note="residues 1 to 505 of 622 |
| CDS | 5573..7441 | |

are 83.96 pct identical to residues 1 to 505 of 519 from E. coli K12 : B3747; residues 1 to 622 of 622 are 84.72 pct identical to residues 1 to 622 of 622 from GenPept : >gb|AAL22738.1| (AE008881) KUP family, potassium transport system, low affinity [Salmonella typhimurium LT2]
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 IAVTGTMVITSILFCVAKWNHW
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 LSFLGLVMPFIIMTTWKSERFSLLRR
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 TMRITDDPVYVHNVERVTIBQLSPTFWRVVARYGW
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 /locus-tag="y0007"
 /function="transport; transport of small molecules; carbohydrates, organic acids, alcohols"
 /note="residues 1 to 139 of 139 are 68.34 pct identical to residues 13 to 151 of 151 from E. coli K12 : B3748"
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 membrane-associated protein"
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 TDQIVIGDAGLIPATTTRIDLAL
 TRGVPGFLQVVDVVTQEMQVENAYLAEEIVKNNP
 QLHEALVLLTQLEQRQENQIALR
 YISHEAFKEQTQCSRRAVIRSGECSPFANIILGSG
 VTF"
 /gene="rbsK"

CDS 8116..9042 /locus-tag="y0008"
/gene="rbsK"
/locus-tag="y0008"
/function="enzyme; degradation of
small molecules; Carbon compounds"
/note="residues 4 to 307 of 308
are 71.38 pct identical to
residues 5 to 308 of 309 from E.
coli K12 : B3752; residues 1 to
308 of 308 are 100.00 pct
identical to residues 1 to 308 of
308 from GenPept :
>emb|CAC88875.1| (AJ414141)
ribokinase [Yersinia pestis]"
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/locus-tag="y0009"
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/note="residues 6 to 46 of 67 are
56.09 pct identical to residues
194 to 234 of 330 from GenPept :
>gb|AAK16096.1|AF288084-2
(AF288084) NgrF [Photorhabdus
luminescens]"
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CDS 9062..9265 /locus-tag="y0009"
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194 to 234 of 330 from GenPept :
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(AF288084) NgrF [Photorhabdus
luminescens]"
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gene complement(9262..10686) /locus-tag="y0010"
CDS complement(9262..10686) /locus-tag="y0010"
/function="putative transport"
/note="residues 3 to 465 of 474
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residues 4 to 466 of 475 from E.
coli K12 : B3754; residues 3 to
465 of 474 are 74.08 pct identical
to residues 4 to 466 of 475 from
GenPept : >gb|AAL22745.1|
(AE008881) putative MFS family
transport protein (1st module)
(Salmonella typhimurium LT2)"
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TTWHWIFILNIPIGLLGLIFYARKYMPNFTMPKRT
FDFVGFLLFGISLVMISTSLEIMG
RPEIADYLPAATLLGGMLIIFYIFHAKGHPNPL
IGLPLFKTRTFSGVIAGNVASRLG
TGCVPFLMLMLOVGFGBYALIAGCMMAPTAIGS
IMAKSAVTQVLRSLSGYRKVLVAGIT
LIIGVLIASFALQSPGMSAWMMILPLFILGIAMS
TQFTAMNTITLADLTDNASSGNS
VLAVTQQLSISFGIAISATVLRFYDGLSLGGNVD
HFHYTFITMGIVTLLSSLVFLKK
PRDGDNLIQGRNVKVKVAPQVKNNV"

gene complement(10766..11455 /locus-tag="y0011"
)
CDS complement(10766..11455 /locus-tag="y0011"
)
/note="residues 49 to 229 of 229
are 64.08 pct identical to
residues 1 to 180 of 181 from E.
coli K12 : B3755; residues 1 to
229 of 229 are 67.68 pct identical
to residues 1 to 229 of 230 from
GenPept :
>gb|AAG58958.1|AE005607-4
(AE005607) yieP gene product
[Escherichia coli O157:H7 EDL933]"
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EQFGVSRATAVEAKVMLAAKGMLLPRPRIGTRVM
PQTWNWYLDQELLTWWMTKENFDQ
VMQHFLILRTSLEPQACYLAAATHANEKQRELLAS
LVAEMRALHSNFRNREQWIQVDTQF
HKLYIEASNPNFLISFANLFSSVYYSYFRAITGD
EVIKLQHHQNIVDTILAGDNQGAL
FACQVLLKTVD"
gene 12016..13600 /locus-tag="yr001"
rRNA 12016..13600 /locus-tag="yr001"
/gene
/trnA 13694..13766 /product="16S ribosomal RNA"
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/note="anticodon: TTC"
gene 14022..16928 /locus-tag="yr002"
rRNA 14022..16928 /locus-tag="yr002"
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/product="23S ribosomal RNA"
gene complement(17019..17426 /locus-tag="y0012"
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CDS complement(17019..17426 /locus-tag="y0012"
)
/note="residues 48 to 120 of 135

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are 30.00 pct identical to residues 84 to 159 of 443 from GenPept :
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 /db-xref="GI:21956669"
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 CROVNSFLLLPNIHVTGADTQSRTGDLTLTKGA
 LYQLSHISTTKFDQACPTLAWGD
 PTLEPSALRRTISEFGMGSGGTTALWPPGKFCFN"
 gene 17036..17155
 rRNA 17036..17155
 gene 17169..17241
 tRNA 17169..17241
 gene 17285..17399
 rRNA 17285..17399
 gene 18140..19069
 CDS 18140..19069
 gene complement(19262..19411 /locus-tag="y0014")

/locus-tag="yr003"
 /locus-tag="yr003"
 /product="5S ribosomal RNA"
 /locus-tag="yt002"
 /locus-tag="yt002"
 /product="tRNA-Thr"
 /note="anticodon: GGT"
 /locus-tag="yr004"
 /locus-tag="yr004"
 /product="5S ribosomal RNA"
 /gene="metA"
 /locus-tag="y0013"
 /gene="metA"
 /locus-tag="y0013"
 /function="enzyme; amino acid biosynthesis: Methionine"
 /note="residues 1 to 309 of 309 are 79.61 pct identical to residues 1 to 309 of 309 from E. coli K12 : B4013; residues 1 to 309 of 309 are 79.61 pct identical to residues 1 to 309 of 309 from GenPept :
 >gb|AAG59205.1|AE005633-2
 (AE005633) homoserine transsuccinylase [Escherichia coli O157:H7 EDL933]"
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 /protein-id="AAM83609.1"
 /db-xref="GI:21956670"
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 PKKIETENQFLRLSNSPLOVDIQQLLRVDSRESK
 NTPTEHLNNFYCDFEDIQQQNFDG
 LIVTGAPLGLVDFCDVAYWFQIERIIIAWAKEHVT
 STLFVCWAVQAALNILYGIPKMTR
 EVKLSGIYQHQTLTEPLALLTRGFDETFLAPHRSY
 ADFPVEVLQOYTDLDILVSSEEA
 AYLFASKDKRVAFVTGHPEYDVDTLAGEYQRDLA
 AGLNFQVPLNYFPSSDASLRPKAS
 WRSHGHILLFANWLNYVVYQITPFDLRHMNPTLD"

CDS complement (19262..19411 /locus-tag="y0014"
)
/note="residues 7 to 48 of 49 are
33.33 pct identical to residues
512 to 553 of 1005 from GenPept :
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(AF165818) hypothetical protein
[Guillardi theta]"
/codon-start=1
/transl-table=11
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/protein-id="AAM83610.1"
/db-xref="GI:21956671"
/translation="MSLPVKKAEEFYGYFSPDRNK
NNQLIHKIKNDHFHYGNIFLIFIY HIVNI"

gene 19456..21087
CDS 19456..21087
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/function="enzyme; central
intermediary metabolism:
Glyoxylate bypass"
/note="residues 12 to 543 of 543
are 79.54 pct identical to
residues 1 to 533 of 533 from E.
coli K12 : B4014"
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/db-xref="GI:21956672"
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EITGPVERMVINALNANVVKVFADFEDESLAPSW
DKVIDGQINLHDAVKGTISYTNES
GKVYOLKPNPAVLIAVRVGLHLPEKHVKWQDEAI
PGLGLDFALFYHNYQQLLAKGSG
PYFYLPKMQSYYQEAAWWSDFVNFTEQRFGLSQGT
IKATVLIETLPAVFQMDIELYHLR
HHIVGLNCGRWDYIIFSYYIKTLKNHHPDRVLPRDQS
VTMNPFLSAYSRLLIKTCHKRGA
LAMGGMAAFIPDKDAEKNKVLVDKVRADKELEAS
NGHDGTVVAHPLGADTVMDVFNKV
LGSRPNQLEVSRSEQDKPITAELLEPCSGERTEA
GMRANIRVAVQYIEAWISGNGCVP
IYGLMEDAATAEISRTSIWQWHHQKSLSNGQT
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FDRGRFEEAARLMERITTQDELIDFLTPGYALL
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/gene="aceA"
/locus-tag="y0016"
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/function="enzyme; central
intermediary metabolism:
Glyoxylate bypass"
/note="residues 4 to 435 of 435
are 85.18 pct identical to
residues 3 to 434 of 434 from E.
coli K12 : B4015; residues 1 to

435 of 435 are 100.00 pct
 identical to residues 1 to 435 of
 435 from GenPept :
 >emb|CAC93193.1| (A414158)
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 pestis]
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 /db-xref="GI:21956673"
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 LQQAKAGVEAIYMSGWVQAADANT
 ASSMYPDQSLSYPVDSVPAVVKRINNSFRRADQIQ
 WSNQIEPGSKGYTDYFLPIVADAE
 AGFGGVNLNAFELMKAMIEAGAAGVHFEDQLAALK
 KCGHMGGKVLPQTQEAIQLVAAAR
 LAADVLGVPTLLIARTDADAADLLTSDCPDYDRE
 FITGDRTAEGFFRTRAGIEQAI
 GLAYAPYADLVWCETSTPDLALAKRFADAVHAQF
 PGKLLAYNCSPSFNNKKNLTDQOII
 ASFQDELSAMGYKYQFITLAGIHSMWNFMFDLAH
 AYAQCSEGGMKHVEKVVQPEFASVD
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 TGSTEEQQF"
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 /locus-tag="y0018"
 /function="enzyme; central
 intermediary metabolism;
 Glyoxylate bypass"
 /note="residues 5 to 572 of 575
 are 75.52 pct identical to
 residues 5 to 572 of 578 from E.
 coli K12 : B4016; residues 5 to
 572 of 575 are 75.88 pct identical
 to residues 5 to 572 of 578 from
 GenPept :
 >gb|AAG59208.1|AE005633-5
 (AE005633) isocitrate
 dehydrogenase kinase/phosphatase
 [Escherichia coli O157:H7 EDL933]"
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 kinase/phosphatase"
 /protein-id="AAM83613.1"
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 LARVKEIYTGLPDYPRFEIAESF
 FNSVYCRFLKHRDLTDPDKLFVFSSQPERRFREIP
 RPLARDFIPKGDLGMLQMLVNLNDL
 SRLHWENLSRDIRYIVMAIRQAFTDEQLASAHF
 QIANELFYRNKAAWLVGKRLRNGD
 IYPFLPLPIHNESGEFLFIDTCLTSKAEASIVFGF
 ARSYFMMVVPLPAAMVEWLREILP
 GKSTAELYTAIGCQKHGKTESYREYLAFIHQSSE

QFIIAPGVKGVMVLVFTLPSFDRV
 FKVIKDFQAPQKEVTQARVLECYQLVKHEHDRVGR
 MADTQEYENFVIDKHRISEPLLAE
 LQHEVPKEKLEDLGDKIVIKHLYMERRMTPLNLYM
 EQADDQQLKDAIEEYGNAIKQLAA
 ANIFFGDMLFKNFGVTRHGRVVFYDYDEICYMTE
 VNFRDIPPPRYPEDEMASEPWYSV
 SPNDVPEEFRRFLCSDRKVRHFEEMHGDLFQA
 SYWRGLQQRIRDGHVEDVFAYRRK
 QRFSQRALN"
 gene complement (24077..24214 /locus-tag="y0017"
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 CDS complement (24077..24214 /locus-tag="y0017"
)
 /note="residues 1 to 39 of 45 are
 35.89 pct identical to residues
 160 to 198 of 460 from GenPept :
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 gene product [Drosophila
 melanogaster]"
 /codon-start=1
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 /protein-id="AAM83614.1"
 /db-xref="GI:21956676"
 /translation="MLSSISKNILHMPIPDTLLQ
 AAPITGLEQIAVHLLKKVPDFPVT A"
 gene complement (24361..24954 /gene="iclr"
)
 /locus-tag="y0019"
 CDS complement (24361..24954 /gene="iclr"
)
 /locus-tag="y0019"
 /function="regulator; central
 intermediary metabolism:
 Glyoxylate bypass"
 /note="residues 5 to 192 of 197
 are 78.19 pct identical to
 residues 98 to 285 of 287 from E.
 coli K12 : B4018"
 /codon-start=1
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 /product="repressor of aceBA
 operon"
 /protein-id="AAM83615.1"
 /db-xref="GI:21956677"
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 SGAGKAFLSTLPPDDQLVQLLHKKG
 LHAYTQHTRTNPTSLSKENIALIRKQGYSFDDEEH
 ALGLRCIAACLFDEHHFAAAISI
 SGPISRITDDRVTTEL GALVIHAAKEITQSYGGGT
 GVK"
 gene 25420..29115
 CDS 25420..29115
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 /locus-tag="y0020"
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 /locus-tag="y0020"
 /function="enzyme; amino acid
 biosynthesis: Methionine"
 /note="residues 6 to 1231 of 1231
 are 85.90 pct identical to

residues 1 to 1227 of 1227 from E.
coli K12 : B4019; residues 6 to
1231 of 1231 are 86.14 pct
identical to residues 30 to 1256
of 1256 from GenPept :
>gb|AAL23012.1| (AE008895)
B12-dependent
homocysteine-N5-methyltetrahydrofo-
late transmethylase, repressor of
metE and metF [Salmonella
typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="B12-dependent
homocysteine-N5-methyltetrahydrofo-
late transmethylase, repressor of
metE and metF"
/protein-id="AAM83616.1"
/db-xref="GI:21956678"
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SLSAEINYEAAARLARICADEWSARTPEKPRVAG
VLGPTNRTASISPKVNNDPAFRNVS
FDQIIVEAIRESTRALIEGGVDLIMIETVFTLNAA
KAATFAVESEFVMGVLLFPMISG
TITDASGRTLSQTTAEFYNSLRHVPLSFLGN
ALGPDELRLRQYVAELSRISSEYYVSA
HPNAGLPNAFGEYDLEAKEMAEQIGEWARAGFLN
IVGGCCGTPRHIAAMVNNAVAGVP
PRPLPDIPVACRLAGLEPLTIDANTLFVNNGERT
NVTGSARFKRLIKEEKYGEALDVA
RQQVESGAQIIDIINMDEGMGLDAEAMVRFLNLIA
GEPDIARVPIMIDSSRWDVIEKGL
KCIQKGKIVNSISMKEGVDAFIHHAKLVRRYGAA
MVVMAFDETQADTRARKIEICRR
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YAVDFIEACADIKAAELPHALISGG
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EEKVDIIGLGLITPSLDEMVNVAKEMERQGFTL
PLLIGGATTSKAHTAVKIEQNYSG
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IDWTPFFMTWSLAGKYPRILEDDEV
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FAVTGGLLEEDALADAYDAOHDDYN
KIMIKALSDRLAEAFAYLHERVRKVYWGFPNE
NLSNEELVRENYQGIRPAPGYPAC
PEHTEKGQIWQLLDVETHTGMKLTESAMYAWPGAS
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EDYAARKGMPATAEVERWLAPNLGYDAD"

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/locus-tag="y0021"
CDS complement (29211..34175 /gene="hylA"
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/locus-tag="y0021"
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extracellular functions; secreted
proteins"
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are 42.08 pct identical to
residues 1 to 1604 of 1608 from
GenPept : >gb|AAA50323.1| (M22618)
hemolysin [Serratia marcescens]"
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FNNNNWLLIQQDKGLTANKIQLDLIA
PRIEVGTGMVTSTEAINALSGNNQIISTDGQILESR
QEDHFNRPSTSLLGGWFSSLFSSESE
ESIDGKYLGSMOSGRINLVSTREGSGVKIAGSLN
GSEEINATIKGLQLEAAKLLGGND
ININANSIQAFGNLHKNEDNGGVTQSLERTLQKG
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NKTTKQTLNKTTLAEAGNLGLTAENKITTOGIKA
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GFVQAKEGGIKIDNAISITTTNKVDERTGVAFDIT
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IHNAIAIKLDGGVDKLDSVTQQNTH
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AKQDSLISQVANASPIMSDKIKNKL
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DGQTVKISEADEKKETKDKWWQKGAKSVGKKIKS
AVQDEQVVGGNGSVKANVEVVESQ
GVEEQSAIRGTONVLTIVKGKTDLVGGKISSKNS
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KNATGGITRE"

gene complement (34188..35964 /locus-tag="y0022"
)
/note="hydB; disrupted by frameshift"
/pseudo

gene complement (36445..37830 /gene="lysC"
)
/locus-tag="y0023"

CDS complement (36445..37830 /gene="lysC"
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/locus-tag="y0023"
/function="enzyme; amino acid biosynthesis: Lysine"
/note="residues 14 to 461 of 461 are 81.47 pct identical to residues 2 to 449 of 449 from E. coli K12 : B4024; residues 14 to 461 of 461 are 81.47 pct identical to residues 2 to 449 of 449 from GenPept :>gb|AAAG59223.1|AE005635-3 (AE005635) aspartokinase III, lysine sensitive [Escherichia coli O157:H7 EDL933]"
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/transl-table=11
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MLENIAMLSSEAASLATSPALTDELVSHGELMSTL
LFVELLRQRQVAVENFDVRKVMR
NDRFGRAEPDTISALAEALAQTLAPRIEDAAIVTQ
GFIGSEGKGRTTTLGRGGSQDYTAA
LLGEALNVSRIDIWTDVPGIYTTDPRVPAAKRI
DKIAFEEAAEMATFGAKILHPATL
LPAVRSIDIPMFVGSSKDPAAAGGTLCVNETYNPPL
FRALALRRQTLTTLHSNLMLHAR
GFLAEVFNILARHSISVLDITTSEVSVALTD
GSTSTGDSSLTTSLLTESSLCRV
EVEEDLALVAIIGNNLSQLACGVGKEVFGVLDPFN
IRMICYGASSHNLCFLVPGNDADK
VWQTLHYNLFE"

| | | |
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| gene | 38200..39846 | /gene="pgi"
/locus-tag="y0024" |
| CDS | 38200..39846 | /gene="pgi"
/locus-tag="y0024"
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metabolism, carbon: Glycolysis"
/note="residues 1 to 548 of 548
are 87.40 pct identical to
residues 1 to 548 of 549 from E.
coli K12 : B4025; residues 1 to
548 of 548 are 87.40 pct identical
to residues 1 to 548 of 549 from
GenPept :
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(AE005635) glucosephosphate
isomerase [Escherichia coli
O157:H7 EDL933]"
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isomerase"
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IKSMSGEKINRTEDRVHLIALR
NRSNTIPIVVDGKVMPPEVNAVLAKMKQFCDRVIS
GDWKGYTGKAIDVVVNIGGGSDL
GPYMTVEALRPYKHNLMHFVSNVDGTHIAEALK
PLNPETTLEFLVASKTFTTQETMTN
AHSARDWFLSAAGDPAHVAKHFAALSTNAKAVGE
FGIDINNMEEFWDWVGGRYSLWSA
IGLSIALSVGFEEHFEQLLSSGAHAMDKHFAETPAE
KNLPVLLALIGIWYNNFFGAETEA
ILPYDQYMHRFPAYFQQGNAMESNKGYVDRNGHPV
DYQTGPQIWIWGEPEGTNQHAFYQLI
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QTEALFGKSLEDVEAEFAAGKT
PEQVAHVAFPKVFEGRPTNSILLREITPFLSGA
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REKNWR" |
| gene | 39981..40388 | /locus-tag="y0025"
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| CDS | 39981..40388 | /note="residues 6 to 135 of 135
are 67.69 pct identical to
residues 8 to 136 of 136 from E.
coli K12 : B4030"
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/db-xref="GI:21956683"
/translation="MAKNSRSQWIAKNLQRLLNV
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SGYHFPLRYFIYIGITAIIIRLIIV
DHENPIDTLISGSILVLUVTLYLANTERLKRE" |
| gene | complement(40531..41442) | /gene="malG"
)
/locus-tag="y0026" |

CDS complement (40531..41442 /gene="malG"
)
/locus-tag="y0026"
/function="transport; transport of
small molecules; carbohydrates,
organic acids, alcohols"
/note="residues 8 to 303 of 303
are 88.17 pct identical to
residues 1 to 296 of 296 from E.
coli K12 : B4032; residues 8 to
303 of 303 are 90.87 pct identical
to residues 1 to 296 of 296 from
GenPept : >gb|AAL23051.1|
(AE008897) ABC superfamily
(membrane), maltose transport
protein [Salmonella typhimurium
LT2]"
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/transl-table=11
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of maltose/maltodextran ABC
transporter"
/protein-id="AAM83621.1"
/db-xref="GI:21956684"
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SLRPGNFATGSLIPDQISWEHWKLALGMSVTHAD
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AMGIVALSTTCAYAFARMRFRGKSALLKGMLIFQ
MFPAVLSSLVALYALFDRIGQYMPF
IGLNTHGGVIFAYMMGQIALHVWTIKGYFETIDNS
LEEAALLDGATPWQAFLRVLLPLS
VPILAVVFILSFIIAITEVPVASLLRDVNSYTL
AVGMQQLNPQNYLWGDFAAAALV
SAIPITTFLAQRWLVGGLTAGGVKG"
gene complement (41435..43027 /gene="malF"
)
/locus-tag="y0027"
CDS complement (41435..43027 /gene="malF"
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/locus-tag="y0027"
/function="transport; transport of
small molecules; carbohydrates,
organic acids, alcohols"
/note="residues 18 to 530 of 530
are 75.43 pct identical to
residues 5 to 514 of 514 from E.
coli K12 : B4033"
/codon-start=1
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/product="inner membrane permease
of maltose ABC transporter"
/protein-id="AAM83622.1"
/db-xref="GI:21956685"
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VLMYAQGEYLFIAVTLILIVSLGLYVANRRAYAW
RYVYPGVAGMGLFVLFPLIICIAI
AFTNYSSTNQLTFERAQSVLLDRQFQTGKTFTEG
LYPSDNQWRQLTNPDGSLFISE
PFSFEATGEQKVVMVAPTTAQQTSEPAASLRRIITQS
RQALSSLVAILPDGAELRMSSLRQ

FSGTKPPLYTLGADGKELINQQTGVKYWPNPSTGF
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 WKNFLRVLHDEGIQKPFISIFIWITILFSVMSVT
 TVAVGMVLACVVQWDSLKGKAIYR
 VMLILPYAVPSFISILIFGLFNQSFGEINLMLS
 HLFG1KPAWFSDPITAKSMILIVN
 TWLGYPYMMILCMGLLKAIPDDLYEASAMDAGP
 FQNFFRIFTPLLIKPLTPLMIASF
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 NYTYRVAFEGEGQQDFGLAAIAT
 LIFILVGALAILNLKASKMNF"

| | |
|------|--|
| gene | complement (43199..44410 /gene="male" |
| |) |
| | /locus-tag="y0028" |
| CDS | complement (43199..44410 /gene="male" |
| |) |
| | /locus-tag="y0028" |
| | /function="transport; transport of small molecules; carbohydrates, organic acids, alcohols" |
| | /note="substrate recognition for ABC transporter and chemotaxis; residues 14 to 403 of 403 are 84.61 pct identical to residues 7 to 396 of 396 from E. coli K12 : B4034; residues 7 to 403 of 403 are 84.13 pct identical to residues 4 to 396 of 396 from GenPept : >emb CAD09213.1 (AL627282) periplasmic maltose-binding protein [Salmonella enterica subsp. enterica serovar Typhi]" |
| | /codon-start=1 |
| | /transl-table=11 |
| | /product="periplasmic maltose-binding protein" |
| | /protein-id="AAM83623.1" |
| | /db-xref="GI:21956686" |
| | /translation="MTRSFHKSGIGKTARVLALS
ALTTLVLSAFAKIEEGKLVIWI
NGDKGYNGLAEVGKKFEKDGTGKVTIEHPDKLEE
KFPQVAATGDGPDIIFWAHDRFGG
YAQSGLLAELTPSKAFQEKLFPFTWDAVFRNGKL
IGYPVAVEALSLIYNNKDLVKEAPK
TWEELIPALDKTILRANGKSAIMWNLQEPEYFTWPVI
AADGGYAFKFENGVYDAKNVGVNN
AGAQAGLQFIVDLVKNKHINADTDYSIAEAFNK
GETAMTINGPWAWSNIDKSINKNYG
VTLLPTFHQPSPKFVGVLTAGINAASPNKELAT
EFLENYLITDQGLAEVNKDPRPLGA
VALKSFQEQLAKDPRIAATMDNATNGEIMPNIPQ
MAAFWYATRSVAVLNATGRQTVEA
ALNDAATRITK" |
| | /locus-tag="y0030" |
| | /locus-tag="y0030" |
| gene | 44888..45250 |
| CDS | 44888..45250 |
| | /note="residues 9 to 49 of 120 are 36.58 pct identical to residues 24 to 64 of 604 from GenPept : >gb AAK27723.1 AF358444-1 (AF358444) alpha-glucosidase [Bifidobacterium adolescentis]" |

/codon-start=1
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/product="hypothetical"
/protein-id="AAM83624.1"
/db-xref="GI:21956687"
/translation="MLSARSIPNPALYRIHPVSE
RDGQGNVGVDYRGLNGVCDSSLPC
WISMLRRCSTCSPILRPQQGPCHWLGGTARS
ERVIRALGVNGSCRGLLPLFFFI
QIHMKSCLRKQRSNAWLM"
/locus-tag="y0029"
/locus-tag="y0029"
/note="residues 33 to 76 of 78 are
34.78 pct identical to residues
399 to 444 of 933 from GenPept :
>gb|AAGS1093.1|AC025295-1
(AC025295) auxin response factor 6
(ARF6) [Arabidopsis thaliana]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83625.1"
/db-xref="GI:21956688"
/translation="MRLIITLLDQYVEALFNVQP
YTQAATPSGATLPLAWRHAQRES
HQGTGGNQWVMPGFASITVFLHSDSYEKLFAQAKE
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/gene="malK"
/locus-tag="y0031"
/gene="malK"
/locus-tag="y0031"
/function="transport; transport of
small molecules; carbohydrates,
organic acids, alcohols"
/note="residues 1 to 369 of 369
are 84.90 pct identical to
residues 1 to 371 of 371 from E.
coli K12 : B4035; residues 1 to
369 of 369 are 84.55 pct identical
to residues 1 to 369 of 369 from
GenPept : >gb|AAL23054.1|
(AE008897) bifunctional: ABC
superfamily (atp-bind), maltose
transportprotein; phenotypic
repressor of mal operon
[Salmonella typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="ATP-binding component of
ABC transport system for maltose"
/protein-id="AAM83626.1"
/db-xref="GI:21956689"
/translation="MANVTLSSVYKAFGEAVISR
DINLEIDDGEGFVVFGPSGGKST
LLRMIAGLEDITSGELLIGGKRMNEVPSSERGIG
MVFQSAYALPHLSVAENMSFGLKL
AGVKKAEIYQRVNQVAEVQLQLAHLLDRRPKALSG
GQRQRVAIGRTLVSEPDVFLDEP
LSNLDAALRVQMRIEISRLHKRLERTMITYVTHDQ
VEAMTLADKIVVLDAIGNIAQVGKPK
LELYHYPAHRVAGFIGSPFKMNFLPVKVTAEEPR
QVQIELPNHQRVWLPVEGDQVQVG

ANMSLGIIRPEHLLPSSAESTVLEGEIIVVEQLGN
 ETQIHIIQIPAIRQNLVYRQNDDVVL
 VEEGATFSIGLPPHRCHLFREDGTACKRLYQELG
 V"
 gene 46250..47689
 CDS 46250..47689

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/gene="lamB"
/locus-tag="y0032"
/gene="lamB"
/locus-tag="y0032"
/function="transport of small
molecules; carbohydrates, organic
acids, alcohols"
/note="defective for phage lambda
uptake; residues 83 to 475 of 479
are 87.96 pct identical to
residues 2 to 400 of 400 from
GenPept : >gb|AAA70348.1| (U16150)
malto porin [Yersinia
enterocolitica]"
/codon-start=1
/transl-table=11
/product="maltose high-affinity
receptor"
/protein-id="AAM83627.1"
/db-xref="GI:21956690"
/translation="MOHSFSPVCHRIGVTSSVRMA
LHVSGCTKNWASSYGDAWLQRMK
RMPTGKYNRRLIMITLRKLPIALAVAAGVLSTQA
MAVDFHGTYARSGIGWTASCGEQQC
FQTTGAQSKEYRLGNECETYAEKLKGQELWKEGDK
SFYLDTNVAYSVSQRDWESTDPA
FREANVQGKNLIESLPGSTIWAGKRFYQRHDVHM
IDFYWWDISGPAGALETIDLGFGK
LSVAATRNSESGGSSAWIDNQRENAYTIINNVYD
VRLAGLETNPGGSLELGVDYGRAD
TQEGLSPLAPNAKDGVMLTAEHTQSLMGGFNKFV
VQYATDMSITYNTIGHSQGTSVNNN
GHLLRVIDHGAINLAEKWDMMYVALYQDIDLDDNN
NGNTWYSVGVRPMYKWTPIMSTLL
EAGYDNRVKSGHTGERNGQYKLTILAQQWQAGDSIW
SRPAIRVNFATYANDEKNGYSDTT
GVAQDGTTGIGTNSRGKNNEVTFGAQFEAWW"
/gene="malM"
/locus-tag="y0033"
/gene="malM"
/locus-tag="y0033"
/function="phenotype; degradation
of small molecules; Carbon
compounds"
/note="residues 7 to 309 of 309
are 51.80 pct identical to
residues 3 to 306 of 306 from E.
coli K12 : B4037; residues 7 to
309 of 309 are 50.98 pct identical
to residues 3 to 305 of 305 from
GenPept : >gb|AAL23056.1|
(AE008898) periplasmic protein of
mal regulon [Salmonella
typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="periplasmic protein of
mal regulon"

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/protein-id="AAM83628.1"
/db-xref="GI:21956692"
/translation="MYEGITMKNLLSCLVLAL
GGTAPLAVQAASITSPANVSIAPT
ISTTLLQQLPWQPLVPPVTQDIOLTAGSPHISQG
EVEGAVAAFALPADRGSLEVTLSS
LLTDKQLFTPSVLVLD EQMRPAAYYPSSYFTYEK
AGIMINNDRLQGVMLTPALGQKQI
YLLVYTTRDQLKTTQLLDPAKAYAQGVGVNAVPD
IPDELVNHSPGTGLRKVTSSEQGM
GNIMIGLIQSAPTSAPVVVGSSIQPVAAPQSEPA
KPAAPMLGETENYFNQAIKDADVKA
GDVDKALKLNLNEAEHLGSTSARKTFIGSVKGKG"
gene complement(49078..49236 /locus-tag="y0034"
)
CDS complement(49078..49236 /locus-tag="y0034"
)
/ note="residues 5 to 52 of 52 are
34.00 pct identical to residues
508 to 557 of 597 from GenPept :
>gb|AAF30492.1|AE002108-5
(AE002108) DNA polymerase III
gamma-tau subunits [Ureaplasma
urealyticum]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83629.1"
/db-xref="GI:21956693"
/translation="MTKVAIIGVVNLFDVTHL
CINKYCKSFSLCSQIPIERKPKNL NVILNKKE"
/locus-tag="y0035"
/locus-tag="y0035"
/ note="residues 37 to 95 of 116
are 39.39 pct identical to
residues 12 to 74 of 476 from
GenPept : >emb|CAC05244.1|
(AL391604) DNAJ domain protein
similar to human tetratricopeptide
repeat protein and protein kinase
inhibitors [Schizosaccharomyces
pombe]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83630.1"
/db-xref="GI:21956694"
/translation="MTLNNTGSSLVVEKNPVGNF
LKFAMNFPNLLLFSDGTLLIKQVE
RELKTHLICNEFVKNSKIVTVYITLGNDALLI
YYSNRNFYKKSYIKCGDIACMNYT
VNEGYLTTIEILWR"
gene complement(49742..50260 /locus-tag="y0036"
)
CDS complement(49742..50260 /locus-tag="y0036"
)
/ note="residues 1 to 172 of 172
are 80.23 pct identical to
residues 1 to 172 of 172 from
GenPept :
>gb|AAG54535.1|AE005199-5
(AE005199) Z0266 gene product

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| | | |
|--|--|------------------------------------|
| | | [Escherichia coli O157:H7 EDL933]" |
| /codon-start=1 | | |
| /transl-table=11 | | |
| /product="hemolysin co-regulated protein" | | |
| /protein-id="AAM83631.1" | | |
| /db-xref="GI:21956695" | | |
| /translation="MPTPAYISITGKTQGNITAG | | |
| AFTAESVGNIVYVGHEDEMVLVQEFT | | |
| EHIVTVPTDPQSQQPSGQRRAHKEPLRFTVAYNKAV | | |
| PLLYNALASGEMLPTVELKWKYRTS | | |
| IEGKQEHFTTAKLEDATIIDIICKMPHCQDSTKA | | |
| EFTQLVRVSLAYRKINWDHTTAGT | | |
| SGADDWRAPIEA" | | |
| /locus-tag="y0037" | | |
| /locus-tag="y0037" | | |
| /note="residues 2 to 166 of 166 | | |
| are 62.65 pct identical to | | |
| residues 1 to 166 of 166 from | | |
| GenPept : | | |
| >gb AAG54533.1 AE005199-3 | | |
| (AE005199) Z0264 gene product | | |
| [Escherichia coli O157:H7 EDL933]" | | |
| /codon-start=1 | | |
| /transl-table=11 | | |
| /product="conserved hypothetical protein" | | |
| /protein-id="AAM83632.1" | | |
| /db-xref="GI:21956696" | | |
| /translation="MMSKNKQSSVAPKERINIKY | | |
| VPNTGDQVAEIELPLNLVUVGDLK | | |
| GVREETSIEEROVVSVNKNNFNSVMNEANISLSF | | |
| NVPNRLEGDEMDPVALSIKGLD | | |
| DFSPDNVAKVPELKILREALVALKGPLGNI | | |
| PAFRSRLQDLLQEDMREQLLKEL DILNQK" | | |
| /locus-tag="y0038" | | |
| /locus-tag="y0038" | | |
| /note="residues 20 to 492 of 493 | | |
| are 76.95 pct identical to | | |
| residues 19 to 491 of 492 from | | |
| GenPept : >gb AAF96022.1 | | |
| (AE004353) conserved hypothetical protein [Vibrio cholerae]" | | |
| /codon-start=1 | | |
| /transl-table=11 | | |
| /product="hypothetical" | | |
| /protein-id="AAM83633.1" | | |
| /db-xref="GI:21956697" | | |
| /translation="MPLHEENTVLAAEPASATFL | | |
| LDEIMSQTRMAPGNGDYDIAKQGV | | |
| AAFISSILDGTNEEPINKLLVDRMIELDKKLS | | |
| AQMDEILHANEFRTEIESWRSLSKL | | |
| LVDTDTDFRENKINIMHATKEELLEDFEFSPEII | | |
| QSGFYKHVSSGYGQFGGEPTAAI | | |
| IGNYAFNNSSPDMKLLQYVSAVGAMAHAPFLSSV | | |
| APDFFGIISSFTELPAIKDLKSVE | | |
| GPAHTKWRALRESEDSRYLGLTTPRELLRLPYST | | |
| VENPIKFNYYEDVSRNHEHFLWG | | |
| NTAFLLASCLTDSFAKYRWCPNIIQGPQSGGTVHD | | |
| LPVHLYEAMGQIQAQIPTEVLIID | | |
| RREFELAEEGFITLTMRKGSDNAAFFSANSVQKP | | |
| KVFPNTREGKMAETNYKLGTQLPY | | |

MFVINRLAHYIKVLQREQIGSWKERQDLERELNI
 WLKQYIAQDENPTDVRSSRPLRS
 AQIQVLDVEGDPGWWYQVAMQVRPHFKYMGASFEL
 SLVGRLDKE"
 gene 52837..53277 /locus-tag="y0039"
 CDS 52837..53277 /locus-tag="y0039"
 /note="residues 11 to 140 of 146
 are 35.87 pct identical to
 residues 8 to 134 of 137 from
 GenPept :
 >gb|AAG54530.1|AE005198-11
 (AE005198) Z0261 gene product
 [Escherichia coli O157:H7 EDL933]"
 /codon-start=1
 /transl-table=11
 /product="hypothetical"
 /protein-id="AAM83634.1"
 /db-xref="GI:21956698"
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 EVLNNSRPGACQSAVDLGVIDLNATATSSDFRKSL
 IEKAIKDCIENYEPRISAVTVQLS
 LNHGDPLQLSFHISARVNFFDMGDDVVEFNLQDN
 NRRYCFNQET"
 gene 53277..54503 /locus-tag="y0040"
 CDS 53277..54503 /locus-tag="y0040"
 /note="residues 4 to 365 of 408
 are 49.58 pct identical to
 residues 5 to 367 of 616 from
 GenPept :
 >gb|AAG54529.1|AE005198-10
 (AE005198) Z0260 gene product
 [Escherichia coli O157:H7 EDL933]"
 /codon-start=1
 /transl-table=11
 /product="hypothetical"
 /protein-id="AAM83635.1"
 /db-xref="GI:21956699"
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 AAIERPHLAAFLSEQGSDPDVERL
 LEGFAFLTGNLREKIDQDFPFLTHGLNNMLWPNY
 LRPIPMSMIIYEYPDESVVTEATL
 VKRGSQVMSIPIAQNGQRSAFINSNAHGPQCTF
 TLCRDVWLFPMSIREISANSNEQ
 GILSIHFAAKAELNLQDLDLKLRLRFYLGEDNYTS
 TQLYFWINHYFERAELVNVGNTIP
 MPDFDFNPVGFERDDALPYPKNAYMGYRILQEY
 FCFPEGFLFFDVNGVVDFPPHLNA
 SEFSLNLYFSQALPFEVKVRSTTLRMNCTPAVNL
 FQHDSEAIIDLQGTQTEYPLCVSYH
 NPDHYDIFSVDRVDSWLSKEGVPKGRGRALNPKT
 WTSALLFYLSPVFCRTHSACFQA
 NALCIVIMDIFYNVTL"
 repeat-region complement(54361..54622 /note="insertion element; partial"
)
 /insertion-seq="IS1661"
 gene complement(54393..54650 /locus-tag="y0041"
)
 CDS complement(54393..54650 /locus-tag="y0041"
)
 /function="IS and transposon
 related functions"

/note="IS1661 orfB; residues 5 to
84 of 85 are 60.49 pct identical
to residues 158 to 238 of 240 from
GenPept : >emb|CAA63547.1|
(X92970) orfB [Escherichia coli]"
/codon-start=1
/transl-table=11
/product="putative transposase"
/protein-id="AAM83636.1"
/db-xref="GI:21956700"
/translation="MDHFSSVVDIIRQSMRKGN
CLDNAVMENFFSHLKAEMYHRKKY
DSATVLKRDIVEYIHYYTERISLKTGGMSPAEY
RTQVEKQ"
repeat-region complement(54623..56576 /note="insertion element"
)
gene complement(54689..55471 /locus-tag="y0042"
)
CDS complement(54689..55471 /locus-tag="y0042"
)
/function="IS and transposon
related functions"
/note="IS100; orfB; residues 1 to
260 of 260 are 100.00 pct
identical to residues 1 to 260 of
260 from GenPept : >gb|AAC69770.1|
(AF074612) putative transposase
[Yersinia pestis]"
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/transl-table=11
/product="putative transposase"
/protein-id="AAM83637.1"
/db-xref="GI:21956701"
/translation="MMMELOHQRLMALAGQLQE
SLISAAPALSQAQDVQEWSYMDFL
EHLLHEEKLARHQRKQAMYTRMAAFPAVKTFEY
DFTFATGAPQKQLQSLRSLSFIER
NENIVLGPMSGVKTHLAIAMGYEAVRAGIKVRF
TTAADLLLQLSTAQRQGRYKTTLQ
RGVMAPRLLIIDEIGYLPPSQEEAKLFFFQVIAKR
YEKSAMILTSNLPGOWDQTFAGD
AALTSAMLDRILHHSHVQIKGESYRLRQKRKAG
VIAEANPE"
gene complement(55468..56490 /locus-tag="y0043"
)
CDS complement(55468..56490 /locus-tag="y0043"
)
/function="IS and transposon
related functions"
/note="IS100; orfA; residues 1 to
340 of 340 are 100.00 pct
identical to residues 1 to 340 of
340 from GenPept : >gb|AAC13168.1|
(AF053947) putative transposase
[Yersinia pestis]"
/codon-start=1
/transl-table=11
/product="putative transposase"
/protein-id="AAM83638.1"
/db-xref="GI:21956702"
/translation="MTVFETVMEIKILHKQGMSS

RAIARELGISRNTVKRYLQAKSEP
PKYTPRPAVASLLDEYRDYIRQRIADAHYKIPA
TVIAREIRDQGYRGGMILILRAFIR
SLSVPQEQEPAVRFETEPGRQMVDWGTMRNGRS
PLHVFVAVLGYSRMLYIEFTDNMR
YDTLETCRHNARFFFVGVRREVLYDNMKTVVLQR
DAYQTGQHRFHPSLWQFGKEMGFS
PRLCRPFRQTKGVVERMVQYTRNSFYIPLMTRL
RPMGIVTVDETAANRGLRNLHDOVA
NQRKHETIQARPCDRWLEEQQSMIALLPPEKKEYD
VHLDENLVNFDKHPLHHPLSIYDS FCRGVA"

gene 56560..56985 /locus-tag="y0044"
CDS 56560..56985 /locus-tag="y0044"
/function="IS and transposon
related functions"
/note="IS1541a; residues 6 to 141
of 141 are 100.00 pct identical to
residues 17 to 152 of 152 from
GenPept :
>gb|AAL27370.1|AF426171-1
(AF426171) transposase [Yersinia
pestis]"
/codon-start=1
/transl-table=11
/product="putative transposase"
/protein-id="AAM83639.1"
/db-xref="GI:21956703"
/translation="MHRSLHIVFAPKYRRQVFYR
EKRRAIIGSILRKLCCEWKVNILEA
EYCVDHIMLLEIPPKMSVSGFMGYLKKGSSLML
YEQFGDLKEFKYRNREFPCRGGYYVD
TVGKNTARIQEYIKHQLLEEDKMGEQLSIYPGSP
FTGRK"
repeat-region 56575..57091 /note="insertion element; partial"
gene complement(57193..57432 /insertion-seq="IS1541a"
CDS complement(57193..57432 /locus-tag="y0045"
)
/note="residues 1 to 79 of 79 are
75.94 pct identical to residues 3
to 81 of 81 from E. coli K12 :
B3928; residues 1 to 79 of 79 are
77.21 pct identical to residues 1
to 79 of 79 from GenPept :
>gb|AAL22928.1| (AE008891)
putative cytoplasmic protein
[Salmonella typhimurium LT2]"
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/transl-table=11
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/protein-id="AAM83640.1"
/db-xref="GI:21956704"
/translation="MSFEVFEKLEVKVQQAIDTI
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AGSREALVRENENQLKQEQRHVWQDRLRALLGKME
V"
gene 58060..58908 /gene="glpF"
CDS 58060..58908 /locus-tag="y0046"
/gene="glpF"
/locus-tag="y0046"
/function="transport; transport of

small molecules; carbohydrates,
 organic acids, alcohols"
 /note="residues 1 to 282 of 282
 are 82.62 pct identical to
 residues 1 to 279 of 281 from E.
 coli K12 : B3927; residues 1 to
 282 of 282 are 82.62 pct identical
 to residues 1 to 279 of 281 from
 GenPept :
 >gb|AAG59120.1|AE005623-11
 (AE005623) facilitated diffusion
 of glycerol [Escherichia coli
 O157:H7 EDL933]"
 /codon-start=1
 /transl-table=11
 /product="facilitator for glycerol
 uptake"
 /protein-id="AAM83641.1"
 /db-xref="GI:21956706"
 /translation="MSQTASSTLKGQICIAEFLGT
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 EISIIWGLGVAMAIYLTAASIAGHNLPAVTIALW
 LFACFERRKVLPLYIAQVAGAFCA
 AALVYGLYSSLFVDFEQTHQMVRGSTESLQLAGI
 FSTYEPNPHISVVQAFLVETVITAI
 LMCLILALTDDGNGIPFRGPLAPLLIGILIAVIGA
 SMGPLTGFFALNPARDLGPKAFSYL
 AGWGDIAFTGGRDIFYFLVPIFGPPIVGALLGAFG
 YRALIGRHLPCDVCTLEDEESTTI TTERKA"
 gene 59085..60608
 CDS 59085..60608

/gene="glpK"
 /locus-tag="y0047"
 /gene="glpK"
 /locus-tag="y0047"
 /function="enzyme; central
 intermediary metabolism: Pool,
 multipurpose conversions"
 /note="residues 7 to 507 of 507
 are 84.63 pct identical to
 residues 2 to 502 of 502 from E.
 coli K12 : B3926; residues 5 to
 507 of 507 are 84.49 pct identical
 to residues 7 to 509 of 509 from
 GenPept :
 >gb|AAG59119.1|AE005623-10
 (AE005623) glycerol kinase
 [Escherichia coli O157:H7 EDL933]"
 /codon-start=1
 /transl-table=11
 /product="glycerol kinase"
 /protein-id="AAM83642.1"
 /db-xref="GI:21956707"
 /translation="MTTENTTQKKYIVALDQGTT
 SSRAVVLVDHNANIVSVSQREFTQI
 YPKAGWVEHDPMEIWATQSSTLIEVLAKAGINSD
 EIAGIGITNQRETTIVWDKVTKGKP
 VYNAIVWQCRRTADICEKLLKEGLEEYIRHNTGL
 VVDPYFSGTKVKWILDNVEGARER
 AERGELLFGTVDTWLVNNMTQGRVHVTDYTNASR
 TMMFNIRITKEWDRMLKALNIPRA
 MLPEVRPSSEIYGKTNIGGKGTRIPIAQIAGDQ
 QAALEFGQLCVQPQGMANKNTYGTGC
 LLMLNTGEEAVQSTHGLLTTIACGPRGEVNYALEG

| | | |
|------|--------------|--|
| | | AVFIGGASIQWLRDELKLIGDATD
SEYFATVKVNSNGVYVPAFTGLGAPYWDPYARG
AIFGLTRGVNSNHIIIRATLESIAY
QTRDVLDAMQADSGARLKSLRVDDGGAVANNFLMQ
FQADILGTRVERPAIRESTALGAA
FLAGLATGFWDLLDEVKSASKASIEREFRPGIETTE
RDIRYKGWKAVARARDWEHDE" |
| gene | 60737..61855 | /gene="glpX"
/locus-tag="y0048" |
| CDS | 60737..61855 | /gene="glpX"
/locus-tag="y0048"
/function="phenotype; Not
classified"
/note="unknown function in
glycerol metabolism; residues 37
to 372 of 372 are 84.22 pct
identical to residues 1 to 336 of
336 from E. coli K12 : B3925;
residues 37 to 372 of 372 are
84.22 pct identical to residues 1
to 336 of 336 from GenPept :
>dbj BAA09535.1 (D55718) GlpX
[Klebsiella aerogenes]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83643.1"
/db-xref="GI:21956708"
/translation="MRVKRVOLTPLRLQVRKVIE
FLPIFSFSIPQSTGLTMKRELAIE
FSRVTAAALAGYKWLRGDKNAADGAAVQAMRI
MLNQVNIDGRIVIGESEIDEAPML
FIGEHVGIGQGDAVDIAVDPIEGTRMTAMQANA
LAVLAVGDQGQTLHADPMYMEKLV
VGPAAKGAIDLNLPLEQNLNCNIATALNKPLADLT
VITLAKPRHDGIIAAMQQLGVKVF
AIPDGDVAAASILTCTMPESEVDVMYCIGGAPEGVI
SAAVIRALDGMQGRLLPRHQVKG
DSEDNRRIGEQELLRKCSMGIEAGNVQLQGDMAR
NDNVIFSATGITKGDLLEGIYRKG
NMATTEITLLIRGKSRTIRRIRSTHFLDRKDPAHL
EFLL" |
| gene | 62010..62756 | /gene="fpr"
/locus-tag="y0049" |
| CDS | 62010..62756 | /gene="fpr"
/locus-tag="y0049"
/function="enzyme; central
intermediary metabolism: Pool,
multipurpose conversions"
/note="residues 1 to 248 of 248
are 74.19 pct identical to
residues 1 to 248 of 248 from E.
coli K12 : B3924; residues 1 to
248 of 248 are 77.01 pct identical
to residues 1 to 248 of 248 from
GenPept : >gb AAL22924.1
(AE008890) ferredoxin-NADP
reductase [Salmonella typhimurium
LT2]"
/codon-start=1
/transl-table=11
/product="ferredoxin-NADP" |

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reductase"
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/db-xref="GI:21956709"
/translation="MAEWVSGKITHIEHWTDAFL
SLQVNAPVDPFTAGQFAKLALDIN
GERVORAYSYVNAPSNDHNLEFYLVTVPEGKLSPR
LDQLSVGGEVMITKQAGFFVLEE
IPDCDTLWMLATGTAIGPYLSILQEGQDLERFKH
LVLVHAARFAHDLSSLPLMQLQLEQ
RYNGKLRIGTUVSREEPSGLTGKRVPALENGAL
EAAVGLKIDAKDSHVMLCGNPQMV
RDTQQLKEQREMRRKHLRRKPGHMTSEQYW"
gene complement (63097..63597 /locus-tag="y0050"
)
CDS complement (63097..63597 /locus-tag="y0050"
)
/note="residues 23 to 163 of 166
are 66.66 pct identical to
residues 1 to 141 of 146 from E.
coli K12 : B3921"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83645.1"
/db-xref="GI:21956710"
/translation="MVSCDLEVHFAEIMLGKWC
SSMTIQQWCFSFKGRIGRREFWIW
MGLWLLAMLVIFTLAGKEWLPIQSASFALVFLLW
PTAAVVVKRLHDRNKAGWWALLAV
LAWMMLMAGNWQMLTFIWNQWGVGRFIPTLIFVMMF
IDCGAFILGTEDGNRNFGPEAVPVKF FADKAK"
/locus-tag="y0051"
/locus-tag="y0051"
/note="residues 11 to 204 of 204
are 56.18 pct identical to
residues 10 to 193 of 199 from E.
coli K12 : B3920; residues 10 to
203 of 204 are 57.21 pct identical
to residues 7 to 192 of 198 from
GenPept : >gb|AAL22922.1|
(AE008890) putative periplasmic
protein [Salmonella typhimurium
LT2]"
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/db-xref="GI:21956711"
/translation="MRIILLALALLLITFMLITT
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YLLFNAPTFDLTLVKFRESYNRANPTLPIINEFH
ITVKEDSPPLTRAASKINENLYAS
TALEGKTGKIKTLQITYLPPIKGNEEKATAKLLAIN
YMAALMRQFEPTLSVVQQLANVQK
LLTEGKGSPFYAHTIGAIRYVVADNGEKGLTFAV
EPIKLSSEA"
/gene="tpiA"
/locus-tag="y0052"
/gene="tpiA"
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/function="enzyme; energy
metabolism, carbon: Glycolysis"
gene 63700..64314
CDS 63700..64314

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/note="residues 1 to 255 of 255
are 82.35 pct identical to
residues 1 to 255 of 255 from E.
coli K12 : B3919; residues 1 to
255 of 255 are 84.70 pct identical
to residues 1 to 255 of 255 from
GenPept : >gb|AAD16183.1|
(AF098509) triose phosphate
isomerase [Enterobacter cloacae]"
/codon-start=1
/transl-table=11
/product="triosephosphate
isomerase"
/protein-id="AAM83647.1"
/db-xref="GI:21956712"
/translation="MRHPLVMGNWKLNGLSTHMVN
ELIAGLRKELSTVDGCGVVAIPPA
IYLNQAKHELAGSRIALGAQNVDVNLSGAFTGET
SAEMLKDIGAQVIIGHSERRTYH
QESEDELIACKFGVLKEIGLIPVLCLIGESEAEANEA
GQTEAVCAKQLDAVLNTLGVKAPE
GAVIAYEPIWAIGTGKSATPAQAAQAVHKFIRDHI
AKQDAAVAQVIIQYGGSVNDKNA
AELETPQDIDGALVGGSALKADAFAVIVKAAAKA
KKA"
gene complement(65442..66737 /locus-tag="y0053"
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CDS complement(65442..66737 /locus-tag="y0053"
)
/function="regulator"
/note="residues 28 to 405 of 431
are 30.26 pct identical to
residues 4 to 358 of 383 from
GenPept : >emb|CAB87565.1|
(AJ277295) Fld1 protein
[Sphingomonas sp. LB126]"
/codon-start=1
/transl-table=11
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regulator"
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/db-xref="GI:21956713"
/translation="MPKRQVLFKLKLNKITRRN
MQKKNDRNSIKIMQIRACMTCAEQ
GAASLAALNLFRTQSATIRSIRDLEHTLAISLFE
RHAKGMLLTDLGNVILPRARSAME
ELTRIPALLRRQLQQRDDEGIEDLEPTWLFNERRL
QIFLSSLYRQQHALHVQAQLDITQS
AVSAALKVLEKGAGMYLFRTPKGMLPTPAGHEI
APCISRALNALHHIPEEITAHRGD
LTGSVRVGAFLPSRARLLPQAMIKLISRHPGIKI
VTNESEGFTALIAEELRAGDIDFIIG
ALRNEKMLLDIHSSEILFEEELILLARPNHPLSDR
RVKNQELKDIQWVLPNRPNSRHL
LEVAFKCMGLASPQPVVESGDPAVVRALLGSDM
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SSNDK"
/gene 66730..67551
CDS 66730..67551
/note="residues 34 to 272 of 273
are 65.41 pct identical to

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residues 3 to 238 of 244 from
GenPept : >emb|CAC46343.1|
(AL591788) conserved hypothetical
protein [Sinorhizobium meliloti]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83649.1"
/db-xref="GI:21956714"
/translation="MGNKTHYFLIKPCQNPRQL
KQQKKEKDMAMIPQKTAALVVAHS
ADFEVWRAGGAIALHVEQGYQVHIVCLSYGERGES
AKLWRKGDMTEERVKASRHTEAQA
AANVLGASIEFFDMGDYPLRADKESLFRLADVFR
RIQPHFVLTHSLADPYNYDHPLAA
NLAQEARIIAQAEQYRPGAEAIIGAPPVYCFEPHQ
PEQCQGWPKDVLLDITSVWEEKKYAA
IQCMAQGEHLWEYYTRVALQRGVQAKRNIGIAST
KTIIHGEQYQSLFPRVTEEDLS"
/locus-tag="y0055"
/locus-tag="y0055"
/note="residues 6 to 229 of 237
are 61.60 pct identical to
residues 1 to 224 of 224 from
GenPept : >emb|CAB87566.1|
(AJ277295) FldZ protein
[Sphingomonas sp. LB126]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83650.1"
/db-xref="GI:21956715"
/translation="MSLVNMKGVVVTNIERAELA
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QCQPGDVLLVAPTSECHDGFFGDL
LATSLLAARGVVALVGDIGIRDQSQTLERMNFPVWS
RAVVAQGTVKASLGSVNVPVICAG
QLVNPGDIVVADDGVVIVPREQATAIADAAQTR
VDLETSKRQRNLANGEGLGLDIYQMR
APLAKKGLRYVNSLNALKS"
/locus-tag="y0056"
/locus-tag="y0056"
/note="residues 2 to 471 of 475
are 52.20 pct identical to
residues 3 to 471 of 477 from E.
coli K12 : B0770; residues 2 to
471 of 475 are 52.20 pct identical
to residues 3 to 471 of 477 from
GenPept :
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(AE005254) putative membrane pump
protein [Escherichia coli O157:H7
EDL933]"
/codon-start=1
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protein"
/protein-id="AAM83651.1"
/db-xref="GI:21956716"
/translation="MKNKIWKLCILVMIPPLVIF
IPPPEGLTLSWRLSGFYLAAICG

L1LKPFSEAVLLGVGFAGFFLNNTSQILVGYA
 TSTVWLVAFAFGISISFVKTGLGR
 RIAFHMIIRFCGTTLRLGVTATLEFVISPVTPS
 NTARSGGIVFPPIILSVVKALGSEP
 GDTAKAGSYLMSNYYFVFMKVSSFMFITAMAPNL
 LAADFAAKILG1HLDWGVVWALAMV
 VPGLLLLLIVPAVGYYLDKPELKVKDNKKIADEG
 LAELGPITRNEKLLVGIFISALLG
 WALPSLQLQLFGITLKIDATAVAIMAMALCILLG
 VIKWDVVLQNKGAWNLTLLWFGGI
 GLASALSKEKVFDWLANLIQNNVDFGHNPFIALT
 IIGFLSIIIRYFFASASSYAIAML
 PVFLTVGVAGADPMALALVLAATNSYGGALTHY
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 VIATVCFIVTMVGVYVWWQFLGFVK"
 /gene="modA"
 /locus-tag="y0057"
 /gene="modA"
 /locus-tag="y0057"
 /function="putative transport;
 transport of small molecules;
 Other"
 /note="residues 48 to 271 of 272
 are 55.55 pct identical to
 residues 5 to 229 of 230 from
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 (AB050935) Pro₂ protein
 [Pseudomonas straminea]"
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 /transl-table=11
 /product="molybdate-binding
 periplasmic protein precursor"
 /protein-id="AAM83652.1"
 /db-xref="GI:21956718"
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 IVSGLCMSMVSLSATAAPTEVPSDE
 PVTLRISSMATRQFLTEVIAQFAQQSKYQVELE
 SVGGVDAATKRVEAGEAFDVVILSA
 NAIDKLIDSGKILPNSRIDLVKSGVIAVKEGAQ
 IMDVSSSEETVKQAVLAANTIAYST
 GPGVYLTTEVFHWGIAEQIKDRIVKVPVPGVPG
 SLVAKGEVELGFLQLELLHLKGI
 IILGGLPTDIQIMTHFSAGVPLKTNQQKAIVVLL
 DFLASPAAATEAKIKNGMEPI"
 gene complement(70898..71920 /gene="sbp"
)
 /locus-tag="y0058"
 CDS complement(70898..71920 /gene="sbp"
)
 /locus-tag="y0058"
 /function="transport; transport of
 small molecules; anions"
 /note="residues 12 to 340 of 340
 are 83.58 pct identical to
 residues 1 to 329 of 329 from E.
 coli K12 : B3917"
 /codon-start=1
 /transl-table=11
 /product="periplasmic
 sulfate-binding protein of
 sulfate/thiosulfate ABC
 transporter"

/protein-id="AAM83653.1"
/db-xref="GI:21956719"
/translation="MITIIFLRSGSMRKWGVGLS
LLVLASGAMAKDIQLLNVSYDPTR
EFYQEYNQAFSKYWQQQTGDKVTVRQSHGGSGKQ
ATSVINGIEADVVTLALAYDVDAI
AERGRIDKNWIKRLPDNSAPYTSTIVFLVRKGNP
KQIHWDSDLVKPGTSVITPNPKTS
GGARWNLYLAAGYALEHHNNNDQAKAQEFVNALYK
NVEVLDSGARGATNTFVERGIGDV
LIAWENEALLAVNEVNGNGQFDIVTPSVSILAEPT
VSVVVDKVVVKRGTTRDVAADYLKYL
YSPECQOTIAAKNYYRFRDPVVAAKFAKEFPQLKL
FTIDEVFGGWTQAQKTHFATGGVF DEISKR"

gene complement(72108..73091 /gene="pfkA"
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/locus-tag="y0059"
CDS complement(72108..73091 /gene="pfkA"
)
/locus-tag="y0059"
/function="enzyme; energy
metabolism, carbon: Glycolysis"
/note="residues 1 to 327 of 327
are 77.06 pct identical to
residues 1 to 320 of 320 from E.
coli K12 : B3916; residues 1 to
327 of 327 are 79.20 pct identical
to residues 1 to 320 of 320 from
GenPept : >gb|AAD16179.1|
(AF098509) phosphofructokinase
[Enterobacter cloacae]"
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/product="6-phosphofructokinase I"
/protein-id="AAM83654.1"
/db-xref="GI:21956720"
/translation="MVKKIGVLTSGGDAPGMNAA
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LYENRMKKLDRYSVSDMINRGGTFLGSARPFER
DPEVRKVALKNMHERGIDGLVVIG
GDGSYAGADLLTKEGGIHCVGLPGTIDNDVAGTD
YTIGEFTALETVVVIAIDRLRDTSS
SHQRISIVEVMGRYCGDLTLAAAIAAGCFIAIP
EVEFKRDLVAEIKAGIAGKKHA
IVAITEKLDIDSLAKYIEKETGRETRGTVLGH
QRGGAPVAYDRILASRMAYAVDL
LLQDHDKYKGGFCVGVQNEKMWHELISVCIAPEN
KKSFKFEDWYDTAKKLF"

gene complement(73309..74211 /locus-tag="y0060"
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CDS complement(73309..74211 /locus-tag="y0060"
)
/function="putative transport"
/note="residues 1 to 293 of 300
are 78.49 pct identical to
residues 1 to 293 of 300 from E.
coli K12 : B3915; residues 1 to
293 of 300 are 79.86 pct identical
to residues 1 to 293 of 300 from
GenPept : >gb|AAL22901.1|
(AE008889) putative CDF family
transport protein [Salmonella

typhimurium LT2]"
/codon-start=1
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protein"
/protein-id="AAM83655.1"
/db-xref="GI:21956721"
/translation="MDPQYARWVKAALSATALA
SILLIINKFAWWHTGGSVSLLAALV
DSLVDLAAASLTNLFVVRYSLQPADEEHTFGHK
ESLAALAQSFMISGSALFLFTGF
RHLASPEPLQDPSIGIGVTLVALFSTLILVTFQR
WVVRKTHSQAIRADMLYHQSVDLM
NGAILALASWYGFRRADALFALGIGVYILYSA
LRMGYEAVQSLDRALPDDERQQI
IDIVTSWPGVIGAHDLRTRSGQTRFIQLHLEME
DMMPFLMEAHVLAQEVEHALLYRFP
GADVLIHQDPCSVVPKERHAHWEL"
/locus-tag="y0061"
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/function="IS and transposon
related functions"
/note="unidentified IS; residues 2
to 37 of 40 are 47.22 pct
identical to residues 89 to 124 of
253 from GenPept :
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putative transposase [Vibrio
salmonicida]"
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/transl-table=11
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/protein-id="AAM83656.1"
/db-xref="GI:21956722"
/translation="MIFIDDDNIIRTHQHGTGAVS
ESDESIKKHRGVTRQKLISR"
gene complement(74773..75732 /locus-tag="y0062"
)
CDS complement(74773..75732 /locus-tag="y0062"
)
/note="residues 15 to 314 of 319
are 56.00 pct identical to
residues 4 to 287 of 292 from E.
coli K12 : B3411; residues 16 to
319 of 319 are 62.01 pct identical
to residues 6 to 313 of 313 from
GenPept : >gb|AAL23539.1|
(AE006471) putative cytoplasmic
protein [Salmonella typhimurium
LT2]"
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HDALEFKNFMTOPATACDLLEFHLP
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LKTTVGDGYYVALIEHQSSPDKHM
AFRLLMRYIAAAMQSHEAGYDKLPLVPIFLFYHG
MVTPTPYPPMSWLHAFNQPELAGQL
YCGNFPFLDVTVIPDHEIMTHRRIALLELLQKHI

RQRDLSELLDQLVILIASGYTTED
QLKSAINYIIQVGETAEPEVFIRSLAHLRPEHEE
SLMTIAQKLEQKGGEARGIVKGRVE
GRVEGAQETALKIARTMLANGLDRATVMKMTGLS
EEELTQIHH"

gene complement (75777..75953 /locus-tag="y0063"
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CDS complement (75777..75953 /locus-tag="y0063"
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VALMRTHAAPKSPOQ"
/locus-tag="y0064"
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/note="residues 1 to 33 of 35 are
51.51 pct identical to residues
230 to 262 of 326 from GenPept :
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protein [Bacteriophage WPhi]"
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/transl-table=11
/product="hypothetical"
/protein-id="AAM83659.1"
/db-xref="GI:21956725"
/translation="MKQEVKANASGKLFNMNDYGK
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/locus-tag="y0065"
/locus-tag="y0065"
/note="residues 1 to 56 of 67 are
80.35 pct identical to residues
269 to 324 of 326 from GenPept :
>emb|CAB54522.1| (AJ245959) Int
protein [Bacteriophage WPhi]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83660.1"
/db-xref="GI:21956726"
/translation="MLRHTCASHFMMNSRNIIAL
QQILRHANIQPTMAYAH LAPDYLQ
NTVILTPLKGGLAAETRPQSVHT"
gene complement (76049..76252 /locus-tag="y0066"
)
CDS complement (76049..76252 /locus-tag="y0066"
)
/note="residues 51 to 162 of 162
are 62.50 pct identical to
residues 1 to 112 of 122 from E.
coli K12 : B3914; residues 1 to
162 of 162 are 52.46 pct identical
to residues 1 to 156 of 166 from
GenPept : >gb|AAU22900.1|
(AE008889) periplasmic repressor
of cpx regulon by interaction with
CpxA, rescue from transitory
stresses [Salmonella typhimurium
LT2]"

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periplasmic protein of ABC
transporter"
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FAADNTKVTEGYHGDKMMMNKKG
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LDLEDREAMHKLITADKFDEAAVR
AQAEKMSQNQIERHVEAKVRNQMYNLLTPEQKE
ALNKKHQERIEKLQQKPAQPSSA QK"
gene 77048..77770
CDS 77048..77770
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/locus-tag="y0067"
/function="putative regulator"
/note="residues 9 to 238 of 240
are 90.43 pct identical to
residues 1 to 230 of 232 from E.
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/product="transcriptional
regulator in 2-component system"
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/db-xref="GI:21956728"
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ALSQLDSSIDLLLLDIMPRKNGIETLKELRQHH
QTPVIMLTARGSELDRVLGELGA
DDYLAKPFFNDRELVARIRAILRRSNWSEQQNAE
QGAPTELEVVDCLQLNPGRQEASFEG
QPLELTGTETFTLLYLLAQLHGVVSREHLSQEVL
GKRRLTPFDRAIDMHISNLRRKLPD
RKDGLPWFKTLRGRGYLMVSET"
gene 77767..79143
CDS 77767..79143
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/locus-tag="y0069"
/gene="cpxA"
/locus-tag="y0069"
/function="putative regulator;
global regulatory functions"
/note="acting on arcA; residues 1
to 454 of 458 are 80.83 pct
identical to residues 1 to 454 of
457 from E. coli K12 : B3911"
/codon-start=1
/transl-table=11
/product="probable sensor protein,
histidine protein kinase"
/protein-id="AAM83663.1"
/db-xref="GI:21956729"
/translation="MINSLLTRIFAIFWFTLALV
LMLVLMVPKLDSDLRQLTVLLDSEQR
QGTMLEQHIEAELANDPANDLWMWRRLLHRAIEKW
APPGOHLLILVSEGRIGVORQEV
QMVRNFFIGQSDNADQPKKKYGRVEMVGPFSSIRD
GEDNYQLYLIRPANSQDFINLM
FDRPLLLIATMLISAPLLLWLAWSLAKPARKLK
NAADDVARGNLKQHPELESGPQEF
LATGASFVNQMISSLDRMVVAQQRLISDISHELRT

PLTRLQLATALMRRRHGEKGELER
IEMEAQRQLDSMINDLVLSRSQHKNELHREPIKA
DELWSDVLLENAQFEAEQMGTLLVV
TAPPGPWPLFCNPAAALDSALENIVRNALRYSHHH
IAVAFSIDNQGVIIIVDDDPGVS
PEDREQIFRPFYRTDEARDRASGGTGLGLAIVET
AVSQHRGVVKAEADSPLGGLRLIVW LPLHPLKS"
gene complement (78938..79090 /locus-tag="y0068"
)
CDS complement (78938..79090 /locus-tag="y0068"
)
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83664.1"
/db-xref="GI:21956730"
/translation="MGYLRLLPTLDADSPRFQQL
PGPILFLPTDLGLHLYDKMAGIF VHGPGLG"
gene complement (79192..80256 /gene="ada"
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CDS complement (79192..80256 /gene="ada"
)
/locus-tag="y0070"
/function="enzyme; DNA -
replication, repair,
restriction/modification"
/note="residues 6 to 350 of 354
are 52.75 pct identical to
residues 10 to 353 of 354 from E.
coli K12 : B2213; residues 6 to
345 of 354 are 65.58 pct identical
to residues 18 to 357 of 360 from
GenPept : >emb|CAD16277.1|
(AL646070) probable ADA regulatory
of adaptative response contains:
methylated-DNA--protein-cysteine
methyltransferase EC 2.1.1.63
O-6-methylguanine-DNA
transcription regulator[Ralstonia
solanacearum]"
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methyltransferase; transcription
activator/repressor"
/protein-id="AAM83665.1"
/db-xref="GI:21956731"
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QVEKISQACRLIELAETPPKLNEL
AAQLGLSTFYHRLFKAITGLTPKGYANALRSER
IRAOQLSHGGSVTDAIFEAQYNSSS
RFYAQSQQQLGMMTPTRYRKGGCDARLHFADVESS
LGAILVAKSELGVCAILLGDDPVR
LVQQLQDKFPQANLVGGDAEFEQWVAQVVGCVEA
PKLGLNLPLDIRGTAFQQRVWQAL
REIPIGETASYADIASRIGSPTAVRAVAGACAAN
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VERKLRLLEREGVEKEAEDH"
/locus-tag="y0071"
gene 80349..80933

CDS 80349..80933 /locus-tag="y0071"
/note="residues 33 to 194 of 194
are 80.24 pct identical to
residues 1 to 157 of 157 from E.
coli K12 : B3606"
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/transl-table=11
/product="hypothetical protein"
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/db-xref="GI:21956733"
/translation="MLLNFCFTPPLATAALNKG
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AGLDYHEFADIKHHHDYQAFLDSE
KLDSTQPARLFALTTKGTPAHSAVSYQANDYLLF
GPETRGLPAYIILDALPAQQKIRIP
MQADRSRMNLNSNAVSVVVYEAWRQLGYPGALLKE
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gene complement(81056..81880 /gene="cysE"
)
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CDS complement(81056..81880 /gene="cysE"
)
/locus-tag="y0072"
/function="enzyme; amino acid
biosynthesis: Cysteine"
/note="residues 2 to 274 of 274
are 86.08 pct identical to
residues 1 to 273 of 273 from E.
coli K12 : B3607"
/codon-start=1
/transl-table=11
/product="serine
acetyltransferase"
/protein-id="AAM83667.1"
/db-xref="GI:21956734"
/translation="MMSSEELEQVWSNIKSEARA
LAECEPMLASFFHATLLKHENLGS
ALSYILANKLANPIMPAIAIREVVEEAYRSDAHM
IVSAARDILAVRLRDPAVDKYSTP
LLYLKGFGHALQAYRIGHTWLWAQDRKALAIYLQNQ
VSVAFGVDIHPAAATIGCGIMLDHA
TGIVIGETAVVENDWSILQSVTLGGTGKTSGDRH
PKIREGVMMIGAGAKILGNIEVGRG
AKIGAGSVLQLSVPAPTTAACGVPARIVGKPESDK
PSLMDHQHFNGSIQGFYGDGI"
gene complement(82143..83162 /gene="gpsA"
)
/locus-tag="y0073"
CDS complement(82143..83162 /gene="gpsA"
)
/locus-tag="y0073"
/function="enzyme; energy
metabolism, carbon: Aerobic
respiration"
/note="residues 1 to 336 of 339
are 84.52 pct identical to
residues 1 to 336 of 339 from E.
coli K12 : B3608"
/codon-start=1
/transl-table=11
/product="glycerol-3-phosphate

dehydrogenase (NAD+)"
/protein-id="AAM83668.1"
/db-xref="GI:21956735"
/translation="MNTNPASMAVIGAGSYGTAL
AITLARNGHQVVLWGHDPKHIQQL
QQDRCRNRAFLPDAAFDTLRLLETDLACALAASRD
VLVVVPShVFGAVLHQLKPHLRKD
ARIWATKGLAEATGRLLQDVAREVLGEAIPLAV
ISGPTFAKELAAGLPTAIALASTD
VQFSEDLQOLLHCGKSFRVYSNEDFIGVQLGGAV
KNVIAIGAGMSDGIGFGANARTAL
ITRGLAEMTRLGTLGADESTFNGMAGLGLDLVLT
CTDNQSRNRFGIMLGQGLGVKEA
QDNIQQVVEGYRNTKEVLAQRHGVEMPITEQI
YQVLYCHRNAREAAALTLGRTKKD EKIGI"

gene complement (83162..83638 /gene="secB"
)
/locus-tag="y0074"
CDS complement (83162..83638 /gene="secB"
)
/locus-tag="y0074"
/function="transport; protein,
peptide secretion"
/note="may bind to signal
sequence; residues 1 to 158 of 158
are 91.13 pct identical to
residues 1 to 155 of 155 from E.
coli K12 : B3609"
/codon-start=1
/transl-table=11
/product="protein export;
molecular chaperone"
/protein-id="AAM83669.1"
/db-xref="GI:21956736"
/translation="MSEQNNTTEMAFQIQRIOYTKD
ISFEAPNAQPQVFQDQWPQEVKLDL
DTASSQLAEDVYEVVLRVTVTASLGEET AFLCEV
QQGGIFSVAGIEGTQLAHCLGAYC
PNILFPYARECITSLSVRGTFPQLNLAPVNFDAL
FMNYLQQQAEGEVEGVEQRQDA"
gene complement (83726..83974 /gene="grxC"
)
/locus-tag="y0075"
CDS complement (83726..83974 /gene="grxC"
)
/locus-tag="y0075"
/function="enzyme; biosynthesis of
cofactors, carriers: Thioredoxin,
glutaredoxin, glutathione"
/note="residues 1 to 82 of 82 are
78.04 pct identical to residues 1
to 82 of 83 from E. coli K12 :
B3610; residues 1 to 82 of 82 are
85.36 pct identical to residues 1
to 82 of 83 from GenPept :
>gb|AAL22561.1| (AE008872)
glutaredoxin 3 [Salmonella
typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="glutaredoxin 3"
/protein-id="AAM83670.1"

/db-xref="GI:21956737"
/translation="MAKIEEMYTKATCPFCHRAKA
LLNAKGAAFHEIAIDNDPAKREEM
IARSGRTTVPQIFIDGQHIGGCDDLHALDARGGL
DPLL"
gene complement (84093..84527 /locus-tag="y0076"
)
CDS complement (84093..84527 /locus-tag="y0076"
)
/note="residues 2 to 144 of 144
are 65.73 pct identical to
residues 1 to 143 of 143 from E.
coli K12 : B3611; residues 2 to
144 of 144 are 67.83 pct identical
to residues 1 to 143 of 143 from
GenPept : >gb|AAL22562.1|
(AE008872) putative
Rhodanese-related
sulfurtransferases [Salmonella
typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83671.1"
/db-xref="GI:21956738"
/translation="MLQEIMQFISQHPILSLAWV
LLFGAVVTSFKNSLSKVKEVTRG
EATRLINKEDAVVVDIRTREDYRKGHIAN SINLI
PSDIKGNGLGELEKHKTQPIIVVC
AMGTTSRASADMLS KAGFERVFTLKEGIGWSGE
NLPLARGK"
/locus-tag="y0077"
/locus-tag="y0077"
/note="residues 1 to 515 of 515
are 83.30 pct identical to
residues 1 to 514 of 514 from E.
coli K12 : B3612; residues 1 to
515 of 515 are 83.88 pct identical
to residues 1 to 514 of 514 from
GenPept : >gb|AAL22563.1|
(AE008872) phosphoglyceromutase
[Salmonella typhimurium LT2]"
/codon-start=1
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/product="putative
2,3-bisphosphoglycerate-independen
t phosphoglycerate mutase"
/protein-id="AAM83672.1"
/db-xref="GI:21956739"
/translation="MSSTKKPLVLTLILDGYGHRE
EQQDNAILNAKTFVMDVLWQQQPH
TLIAASGLDVGLPDGMGNSEVGHVNGLGAGRIVY
QDLTRLDEIKEIKEGDFFTNTPLTAA
VDNAVKTGKAVHIMGLLSAGGVHSHEDHIMAMVE
LAAKRGATAIYLHAFLDGRDTPPR
SAESSLKRFTAKFAELGNGRIASIIGRYYAMD
NRWDRVOLAYDLLTQAKEYFTADN
AVAGLQAAAYARGENDEFVKPTVIQATGEADAAM
EGDTLIFMFNFRADRARQITRTFVN
AEFDGFKRDVKVVNFQDFIMLTEYAADIKVACAYP
PASLTNTFGEWLMKHDKTQLRISE
TEKYAHVTFYNGGVEEPFKGEDRILINSPKVAT

YDLQPEMSAELTEKLVSAIGSGK
 YDVIICNYPNGDMVGHGTGDYDAAVKAVETLDNCI
 EQVVAAVKAADGQLLITADHGNAE
 QMRDPATGQAHTAHTSLPVPLIYVGNKAVKEVG
 GKLSDIAPMLSMLMEMEPIQEMITG KPLFIVE"
 gene 86481..87851
 CDS 86481..87851
 /locus-tag="y0078"
 /locus-tag="y0078"
 /function="putative membrane"
 /note="residues 39 to 456 of 456
 are 63.39 pct identical to
 residues 24 to 427 of 427 from E.
 coli K12 : B3613; residues 40 to
 456 of 456 are 65.70 pct identical
 to residues 25 to 427 of 427 from
 GenPept : >gb|AAL22564.1|
 (AE008872) paral putative membrane
 protein [Salmonella typhimurium
 LT2]"
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 /transl-table=11
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 protein"
 /protein-id="AAM83673.1"
 /db-xref="GI:21956740"
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 CAGVLLLFSGQAVEFPVAKASENKNQLKTLQQ
 DIAEKEKSVQQOKKQRSSLLDQLK
 QQENTISQTSRSLRETOATIAELSKDIASLTTSI
 EKLQNQQSQQQSILSKQLAAFKQ
 GKHSSLQLILSGEEESQRSERILAYFSYLNEARQK
 AIEELKQTRTTLSAEKKMLEQKON
 QHKALLDEQKAAQQKLEQARIARQKTLTSLEASL
 EKDQOSLAELKLNESSLRQDQIAKA
 EREAKARAERAKEAARVREREQVKVKEQQAKKTGS
 SYKPSESESRSIMARTGGLGRPGGG
 ALWPVRGNVSHRFGEFLQGELRWKGMVITAPEGS
 EVKAIADGRVLLADWLQGYGLVVV
 IEHKGKGDMSLYGYNQSAVNNGAQVKAGQPIALV
 GTSGGQEPSPLYFEIRROQQAVNP QFWLGR"
 gene 87875..88809
 /locus-tag="y0079"
 /note="disrupted by frameshift"
 /pseudo
 gene complement(88947..89972 /gene="tdh"
)
 /locus-tag="y0080"
 CDS complement(88947..89972 /gene="tdh"
)
 /locus-tag="y0080"
 /function="enzyme; degradation of
 small molecules; amino acids"
 /note="residues 1 to 341 of 341
 are 92.08 pct identical to
 residues 1 to 341 of 341 from E.
 coli K12 : B3616"
 /codon-start=1
 /transl-table=11
 /product="threonine dehydrogenase"
 /protein-id="AAM83674.1"
 /db-xref="GI:21956741"
 /translation="MKALSKLKAEEGIWMTDVPQ
 PELGHNDIMIKRKTAICGTDVHI"

YNWDEWSQKTI PVPVMVGHEYVGEVVAI GQEVKG
 FNIGDRVSGEGHITCGHCRCRGG
 RTHLCRNTVGVGNRPGSFAEYLVIPAFNAFKIP
 DNISDELAIAIFDPFGNAVHTALSF
 DLVGEDVLVSGAGPIGIMAAAVCKHVGARHVIA
 DVNEYRLLDARKMGVTRAVNVSKE
 NLNDVMTTELGMTEGFDVGLEMSGAPPFRSLLNS
 MNHGRRIAMLGIPPSDMSIDWNQV
 IFKGLFIIKGIGYGREMFETWYKMAALIQSGLDLTP
 IIITHRFPIDEFQQGFDAMRSKGSG KVVLSDW"

 gene complement(89982..91223 /gene="kbl"
)
 /locus-tag="y0081"

 CDS complement(89982..91223 /gene="kbl"
)
 /locus-tag="y0081"
 /function="enzyme; central
 intermediary metabolism: Pool,
 multipurpose conversions"
 /note="residues 20 to 413 of 413
 are 84.77 pct identical to
 residues 5 to 398 of 398 from E.
 coli K12 : B3617"
 /codon-start=1
 /transl-table=11
 /product="2-amino-3-ketobutyrate
 CoA ligase (glycine
 acetyltransferase)"
 /protein-id="AAM83675.1"
 /db-xref="GI:21956742"
 /translation="MOLPILEITEMSLPCNKHPF
 YQLEQQLDTTRTEGLYKNERVIT
 SAQQANIAVADGSRVINFCANNYGLGANHPKLIA
 AAKAGMDSHGFMASVRFICGTD
 IHKELEHKLASFLGMEDAILYSSCFDANGGLFET
 LLGPEDAIIISDALNHASIIDGVRL
 CKA KRYRYANNDMTELEIQLQKQAKAEGARHIMIA
 TDGVFSMDGVIANLKVCDLADYE
 QALVMVDDSHAVGVIGANGRRGTHEYCEVMDRVDI
 ITGTILGKALGGASGGYTAGRKELV
 EWLQRSRPYLFSNSLAPAIVASIEVLSLLEEG
 GALDRILWANARLFREKMSAAGFT
 LAGADHAIIPVMLGEAKLQAQDFANALLKEGIYVT
 GFFFVVPKGQARI RTQMSAGHTT
 EQVERAEAFVRIGQLNVIA"

 gene 91394..92371 /gene="rfaD"
 /locus-tag="y0083"

 CDS 91394..92371 /gene="rfaD"
 /locus-tag="y0083"
 /function="enzyme; surface
 polysaccharides and antigens"
 /note="residues 16 to 323 of 325
 are 83.11 pct identical to
 residues 1 to 308 of 310 from E.
 coli K12 : B3619"
 /codon-start=1
 /transl-table=11
 /product="ADP-L-glycero-D-mannoheptose-6-epimerase"
 /protein-id="AAM83676.1"
 /db-xref="GI:21956744"
 /translation="MCGGTQPRKLARVNMTIIVT

GGAGFIGSNIVKALNNIGYKDILV
 VDNLKDGTKFVNLDIADYMDKEDFVASIVAG
 DDMGDIDIAIFHEGACSSSTEWDGK
 YMMDDNNYQYSKDLHFCFLDRSIPFLYASSAATYG
 GRTDNFIEDRQEQLPNVVGYSKF
 LFDQYVREILPQADSQICGFRYPNVYGPREGHKG
 SMASVAFHLLNQINAGERPKLFAA
 SENFKRDFIYVGDVADVNWLWFQNGVSGIFNCGT
 GRAESFQAVADAVVYHQSGPVEY
 IEFPEKLKGRYQAYTOADLTKLRAAGYGPFKTV
 AEGVKEYLAWLNRSV"
 /locus-tag="y0082"
 /locus-tag="y0082"
 /note="residues 5 to 33 of 75 are
 48.27 pct identical to residues 94
 to 122 of 182 from GenPept :
 >dbj|BAAL1839.1| (D83187) delta
 9-fatty acid desaturase [Yarrowia
 lipolytica]"
 /codon-start=1
 /transl-table=11
 /product="hypothetical"
 /protein-id="AAM83677.1"
 /db-xref="GI:21956745"
 /translation="MOVKGLSYSRVAKTLNVISF
 MWVMLLTICGSGKTAYPVFSTAV
 LAGQSLSRLSLMOWWIIKVGQSNTSSLKN"
 /gene="rfaF"
 /locus-tag="y0084"
 /gene="rfaF"
 /locus-tag="y0084"
 /function="putative enzyme;
 macromolecule metabolism:
 Lipopolysaccharide"
 /note="lipopolysaccharide core
 biosynthesis; residues 5 to 351 of
 358 are 73.77 pct identical to
 residues 1 to 347 of 348 from E.
 coli K12 : B3620; residues 5 to
 351 of 358 are 78.38 pct identical
 to residues 1 to 347 of 348 from
 GenPept : >gb|AAL23754.1| (U52844)
 heptosyltransferase II WaaF
 [Serratia marcescens]"
 /codon-start=1
 /transl-table=11
 /product="ADP-heptose--lps
 heptosyltransferase II"
 /protein-id="AAM83678.1"
 /db-xref="GI:21956746"
 /translation="MINGMKILVIGPSWVGDMMM
 SQSLYRTLKAEPAAIDIVMAPAW
 CRPLLARMPEVRHAIPMPLGHGAFAFERRRLGL
 ALRETEYDRAYVLPNSFKSALIPY
 FSGIKRIGWRGEMRYFLNLNDLRLIDKQAFPMMV
 QRYVALAYDKERIRSAADLPQPLL
 WPOLOVRDEEIAETTASFNLTDNRPIIGFCPAGAE
 FGPAKRPHYHYATLAQKLIDDGY
 QVILFGSAKDNNEAGEDIRQALSSTDREYCLNLAG
 QTSLEQAVVLLAACSAVVSNDSGL
 MHVAALNKPLVALYGPSSPDFTPLSEKATVIR
 LITGYHKVRKGDSAQGYHQLSLIDI

QPEHVMAALEKQLATQECCSVKGKD"
/gene="ffaC"
/locus-tag="y0085"
/gene="rfaC"
/locus-tag="y0085"
/function="enzyme; macromolecule
metabolism: Lipopolysaccharide"
/note="lipopolysaccharide core
biosynthesis; residues 9 to 327 of
329 are 68.33 pct identical to
residues 1 to 319 of 319 from *E.*
coli K12 : B3621; residues 9 to
329 of 329 are 81.30 pct identical
to residues 1 to 321 of 321 from
GenPept : >gb|AAL23755.1| (U52844)
heptosyltransferase I WaaC
[*Serratia marcescens*]"
/codon-start=1
/transl-table=11
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/protein-id="AAM83679.1"
/db-xref="GI:21956747"
/translation="MLSQRGRLMHVLIVKTSSMG
DVLHTLPALTDAANNAIPGIRFDWV
VEEGFSQIPISWHPAVDKVIPVAIRRWRKNWFGSD
TRQERCDFKRVVQQRSYDRVIDAQ
GLIKSALAIIITRAKGTKHGPDCKSAREPFASWFY
NCRHEIDTKQHAVERIRQLFAKSL
GYDKPESYGDYIAAQRFLNQLPADAGQYLVFLHA
TTRDNKHWPESHWVQLIELVQPTG
LKIKLWGAEEHHQRALRLAEHFPHVVEVLPKLSL
QVVAEVLAGAKAVSVDTGLSHLT
AALDRPNITLFGPTDFGLIGGYGKNQIAVISEQK
KMDLSAPTIMARLETTLIS"
/gene="kdtA"
/locus-tag="y0086"
/gene="kdtA"
/locus-tag="y0086"
/function="enzyme; surface
polysaccharides and antigens"
/note="residues 37 to 461 of 461
are 79.76 pct identical to
residues 1 to 425 of 425 from *E.*
coli K12 : B3633; residues 37 to
461 of 461 are 88.47 pct identical
to residues 1 to 425 of 425 from
GenPept : >gb|AAC44432.1| (U52844)
3-deoxy-manno-octulosonic acid
transferase [Serratia marcescens]"
/codon-start=1
/transl-table=11
/product="3-deoxy-D-manno-octuloso
nic-acid transferase (KDO
transferase)"
/protein-id="AAM83680.1"
/db-xref="GI:21956748"
/translation="MNNHGSMWCSALLAGKSLFC
PDMVLFLLIHINEIDRMLLRLYQV
LLYLIQPLIWLRLRLRSRKAPAYRKRWGERYGFC
AGKVAGGIMLHSVSVGETLAAIP
LVRALRHRYPSLPIVTMTPTGSERVQSAFGKD
VHHVYLPYDLPGSVNRFQLDQVNPK

LVIIMETELWPNLINTLHRRKIPPLVIANARLSAR
 SAAGYKKIGSFIRTILQQRITLIAA
 QNQEYGDGRFIELGLKRSQLTVTGSLLKFDISVTPE
 LAARAVTLRRQWAPHRPVWIATST
 HDGEETTILEAHRQLLQQPFTLLLILVPRHPERF
 GKAVENTOKIGLSSYTLLRSKGEVPS
 SSTQVVIGDTMGEMLLYGIAIDLAFVGSSLVERG
 GHNPMLLEAAAHAIPVLMGPHTFNFK
 DICAKLEQAEGGLITVTDTLSLVKEITVLLTDDEC
 RLYYGRHAVDVLLHENQGALQRLHH
 LLEPYLPQRSH"
 /locus-tag="y0087"
 /product="lipopolysaccharide core biosynthesis glycosyl transferase"
 /protein-id="AAC44433.1" (U52844)
 glucosyltransferase [Serratia marcescens]"
 /codon-start=1
 /transl-table=11
 /note="residues 1 to 256 of 260 are 75.78 pct identical to residues 1 to 256 of 257 from GenPept : >gb|AAC44433.1| (U52844) glucosyltransferase [Serratia marcescens]"
 /db-xref="GI:21956749"
 /translation="MGTKKRLSVVMITKNEASLL TDCLASVVADEIIVLDSGSEDET RALAQQFGAKVYSNINWPGYGGKQRQLAQQYASGD YILMLDADERVITEPLKIAIESVLL APEEGAVYSCSRRLFLGLGRFMHRSGWYPDRVTRL YPHHQQYRNNDLNVHESLDGSSAKV IPLAGDLLHHTCRDFFAFQRKQLSYAEAWAIQRH QQGKSCSYFAILSHTLGAFSKTWL LRAGFLDGKQGLLAVVNAQYTFNKYAALWALSH QYQKSEKS"
 /gene="kdtB"
 /locus-tag="y0088"
 /product="putative enzyme of lipopolysaccharide synthesis"
 /protein-id="AAM83682.1"
 /db-xref="GI:21956750"
 /translation="MITKAIYPGTFDPITNGHLD LVTRASAMFSHVILATADSSSKP MFTLDERVALAKKVATAPLNVEVLGFSELMAEFA KKHNNANILVRLGLRSVSDFEYEWQL ANMNRHLMPKLESVFLIPSEKWSFISSSLVKEVA RHGGDITPFLPKPVTKALLAKLA"

gene complement (97393..98202 /gene="mutM"
)
/locus-tag="y0090"
CDS complement (97393..98202 /gene="mutM"
)
/locus-tag="y0090"
/function="enzyme; DNA -
replication, repair,
restriction/modification"
/note="residues 1 to 268 of 269
are 79.85 pct identical to
residues 1 to 268 of 269 from E.
coli K12 : B3635; residues 1 to
268 of 269 are 83.70 pct identical
to residues 1 to 270 of 271 from
GenPept : >gb|AAD28805.2| (U52844)
Fpg [Serratia marcescens]"
/codon-start=1
/transl-table=11
/product="formamidopyrimidine DNA
glycosylase"
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/db-xref="GI:21956751"
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QTILYAVVRNARLRNPFVSDEILTL
SDQPVLSVQRRAKYLLLELPKGWIIHLGMGSGL
RVLSEETAAEKHDHVDLVVSNGKI
LRYTDPRRFGANLWAKDLETSNVLAHLPPEPLSD
EFTAQYLFDKSRNKRTLKPWLMD
NKVVVGVGNIYASESLFAAGILPDRAGSLTDAE
SVLKVATIKAVLLHSIEQQGTTL
DFLQSDDGKPGYFAQELQVYGRAGEPCRCQCCHPIE
IAKRGQRSTFFCRHCQH"
/locus-tag="y0089"
/locus-tag="y0089"
/note="residues 25 to 43 of 52 are
57.89 pct identical to residues
170 to 188 of 433 from GenPept :
>emb|CAB86066.1| (AL163002)
putative protein [Arabidopsis
thaliana]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83684.1"
/db-xref="GI:21956752"
/translation="MLAVAAKERAALPVFRYFNG
MFTLPTWFTRTPIDQLLREIPWF TIRLKQKIT"
gene complement (98285..98452 /gene="rpmG"
)
/locus-tag="y0091"
CDS complement (98285..98452 /gene="rpmG"
)
/locus-tag="y0091"
/function="structural component;
ribosomal proteins - synthesis,
modification"
/note="residues 1 to 55 of 55 are
96.36 pct identical to residues 1
to 55 of 55 from E. coli K12 :
B3636"
/codon-start=1

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/gene="radC"
)
/locus-tag="y0092"
/function="phenotype; Not
classified"
/note="residues 10 to 222 of 222
are 58.21 pct identical to
residues 12 to 224 of 224 from E.
coli K12 : B3638; residues 7 to
222 of 222 are 59.72 pct identical
to residues 6 to 221 of 221 from
GenPept : >gb|AAL22588.1|
(AE008873) putative DNA repair
protein, associated with
replication forks [Salmonella
typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="DNA repair protein"
/protein-id="AAM83686.1"
/db-xref="GI:21956754"
/translation="MDEWIGQVAPREKLLKYGAA
VLTDAILAIFLRTGIPGMHVMKKM
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QIQAIGELACRCFSSHLMRSEVLL
NPGITQKFLQNILSHRREIFLVFLDNQHRVIR
HEEMFTGTISSVEVHPREIVREAL
KVNAALLILAHNNHPSGKAEPSQADRLLTTQVIKA
CSLLDIRVLDHVVGRGECVSFAE RGWL"
/gene="dip"
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/function="phenotype; DNA -
replication, repair,
restriction/modification"
/note="residues 39 to 442 of 443
are 75.18 pct identical to
residues 23 to 429 of 430 from E.
coli K12 : B3639; residues 40 to
442 of 443 are 75.12 pct identical
to residues 1 to 406 of 407 from
GenPept : >gb|AAL22589.1|
(AE008873) flavoprotein affecting
synthesis of DNA and pantothenate
metabolism [Salmonella typhimurium
LT2]"
/codon-start=1
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synthesis of DNA and pantothenate
metabolism [Salmonella typhimurium
LT2]"

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metabolism"
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GKHIVLGISGGIAAYKSPELVRLRLDKGADVRVV
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DLLDPAAEAMGHIELGKWDALVIIAPATADLLA
RMAAGMANDLITTVCLATAAPIA
VPAMNQQMYRAPATQENLQLTSKWGVLLGPDSG
SQACGDIGPGRMLDPQEIVALAYN
HFSAKQDLQHLSVMITAGFTREPLDPVRFISNQS
SGKMGFAIAQALAARGSNVTLLIAG
PVNLSTPEGVKRDVITALEMQAQAVQKIAQQNQI
FISCAAADVADYRAEHVSDEKIKKQG
DEITLKLVKNPDIVAGVASMANKRPFVVGFAET
QNVEEYARQKLARKNLDLICANDV
SLAEHGFSNDTNALHLFWSTGEKRLPLSDKYLLS
QRЛИДЕИВСРҮДЕКНРН"

gene 101008..101478 /gene="dut"
CDS 101008..101478 /locus-tag="y0094"
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/locus-tag="y0094"
/function="enzyme;
2'-Deoxyribonucleotide metabolism"
/note="residues 6 to 156 of 156
are 84.76 pct identical to
residues 1 to 151 of 151 from E.
coli K12 : B3640; residues 6 to
156 of 156 are 85.43 pct identical
to residues 1 to 151 of 151 from
GenPept :
>gb|AAG58784.1|AE005591-8
(AE005591)
deoxyuridinetriphosphatase
(Escherichia coli O157:H7 EDL933)"
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se"
/protein-id="AAM83688.1"
/db-xref="GI:21956756"
/translation="MSAVMMKKIDIKILDPRVGN
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VELQFGQTLLPTGLAIHGDLSALAAILPRSGL
GHKGHIVLGNLVLGLIDSYQGQLM
VSVWNRGQQPFTIEPGERIAQMVFVPPVQAEFNL
VEDFTDSERGTTGGFGHSGRQ"
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/function="putative regulator"
/note="residues 1 to 198 of 198
are 83.33 pct identical to
residues 15 to 212 of 212 from E.
coli K12 : B3641; residues 1 to
198 of 198 are 83.83 pct identical
to residues 1 to 198 of 198 from
GenPept : >gb|AAL22591.1|
(AE008873) putative
transcriptional regulator

gene 101600..102196
CDS 101600..102196

(TetR/ArcR family) [Salmonella typhimurium LT2]
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 PGLTRIMTGHALMFEDRLOGRINQLFERIEMQL
 RQVLREKKLRDGQQFIHDEALLAT
 QLLAFCEGMLSRFVRSEFRCPTQEFDSRNPLIV
 AQLQ"

gene complement(102331..1029 /gene="pyrE"
 78)
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 CDS complement(102331..1029 /gene="pyrE"
 78)
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 /function="enzyme; pyrimidine ribonucleotide biosynthesis"
 /note="residues 1 to 213 of 215 are 85.91 pct identical to residues 1 to 213 of 213 from E. coli K12 : B3642; residues 1 to 213 of 215 are 85.91 pct identical to residues 1 to 213 of 213 from GenPept : >gb|AAL22592.1| (AE008873) orotate phosphoribosyltransferase [Salmonella typhimurium LT2]"
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 KTHGEGGNLVGSPLQGRVMLVDDVITAGTAIRES
 MEIINAQGATLAGVMISLDRQERG
 RGEISAIQEVERDYHCKVIAIVTLNDVIRYLEDK
 PEMAEHLLAVRQYREQYGVTL"

gene complement(103145..1038 /gene="rph"
 61)
 /locus-tag="y0097"
 CDS complement(103145..1038 /gene="rph"
 61)
 /locus-tag="y0097"
 /function="enzyme; degradation of RNA"
 /note="residues 1 to 223 of 238 are 88.78 pct identical to residues 1 to 223 of 228 from E. coli K12 : B3643; residues 1 to 238 of 238 are 100.00 pct identical to residues 1 to 238 of"

238 from GenPept :
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ribonuclease PH [Yersinia pestis]"
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/db-xref="GI:21956760"
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DLKKLGFTITLDCDVLQADGGTRTASISGACVA
LADALNKLVASGKLKANPMKGLVA
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/function="phenotype; Not
classified"
/note="residues 1 to 287 of 287
are 87.45 pct identical to
residues 1 to 287 of 287 from E.
coli K12 : B3644; residues 1 to
287 of 287 are 87.80 pct identical
to residues 1 to 287 of 287 from
GenPept : >gb|AAL22594.1|
(AE008873) putative stress-induced
protein [Salmonella typhimurium
LT2]"
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protein"
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EINPFDILRWPGVMSAEEQDLDIAISTELMQALDT
ALDDFIVSRETEGAALKTLIEQRL
EGVSAEVVKVRAHMPNILQWQRERLLNKLEEAV
QLENTRLEQELVLMQCRIDVAEEL
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/locus-tag="y0099"
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are 74.58 pct identical to
residues 19 to 199 of 223 from E.
coli K12 : B3646; residues 1 to
181 of 207 are 74.58 pct identical
to residues 19 to 199 of 223 from
GenPept :
>gb|AAG58790.1|AE005592-1
(AE005592) orf, hypothetical
protein [Escherichia coli O157:H7
EDL933]"
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CNCIPLVFQEYIAGISFAAAWIY
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gene complement(105890..1075 /locus-tag="y0100"
93)
CDS complement(105890..1075 /locus-tag="y0100"
93)
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are 43.79 pct identical to
residues 3 to 561 of 562 from E.
coli K12 : B3647"
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VAHTGLKKLDETALTRWMAGRKNLWVQPKVDGV
AVTLVYHGGKLVQLLSRGNGVKCQ
NWTEKAPPISAIPQYIANAPALLTLQGEFLLLMD
GHQQAKSGGVNARSTVAGALMRKS
PSPLLAQVGVEIWANWDGFTTMEKVALLQVMGF
PFTAKYSEPVMSHLDVQWRQFWF
QAPLFVTDGVVVRQEEEPAGRYWQATPGQWSMA
WKYPPLQHIAEVKDIHFTLGRTGK
GTVVLEVLPPIKIDDKWIRRNVNIGSVTRWKQWDIA
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LIWLSPGPGGLDIGGIGGGFWQELI
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gene="gmk"
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ribonucleotide biosynthesis"
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are 87.92 pct identical to
residues 1 to 207 of 207 from E.
coli K12 : B3648"
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GRGQDSEEVIKRMEQAVAEMAHY
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CDS 108672..108947 /locus-tag="y0102"
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modification, DNA transcription"
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to 91 of 91 from E. coli K12 :
B3649"
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subunit"
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CDS 108967..111075 /locus-tag="y0103"
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/locus-tag="y0103"
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regulatory functions"
/note="residues 1 to 702 of 702
are 91.45 pct identical to
residues 1 to 702 of 702 from E.
coli K12 : B3650; residues 1 to
702 of 702 are 91.89 pct identical
to residues 1 to 703 of 703 from
GenPept : >gb|AAL22601.1|
(AE008874) bifunctional : (p)ppGpp
synthetase II; also
guanosine-3',5'-bis pyrophosphate
3'-pyrophosphohydrolase
[Salmonella typhimurium LT2];
guanosine-3',5'-bis pyrophosphate
3'-pyrophosphohydrolase"
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 /function="enzyme; DNA -
 replication, repair,
 restriction/modification"
 /note="resolution of Holliday
 junctions, branch migration;
 residues 1 to 693 of 693 are 81.52
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 of 693 from E. coli K12 : B3652;
 residues 1 to 693 of 693 are 81.24
 pct identical to residues 1 to 693
 of 693 from GenPept :
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 helicase, resolution of Holliday
 junctions, branch migration
 [Salmonella typhimurium LT2]"
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 GENIGVELQESLTPVYPTTEGIR
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 PEAIIHLRHP PADIQLADEQQKG
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 WLPERVRYTNA"

gene complement (114221..1154 /gene="glts"
 35)

CDS complement (114221..1154 /gene="glts"
 35)

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 amines"
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 residues 1 to 399 of 401 from E.
 coli K12 : B3653; residues 1 to
 399 of 404 are 82.45 pct identical
 to residues 1 to 399 of 401 from
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 (AJ005339) glutamate permease
 [synthetic construct]"
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 GHGTGAAWSKLFSERYGFENATEV
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 ETIAMISICLMAGNLIAGWLQGTMFELPIFVCVL
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| gene
CDS | 115622..117058
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| gene
CDS | 117206..118915
117206..118915 | |

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 DQTPDRALSLALTGRSVDLNFLHN
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gene complement(119050..1199 /locus-tag="y0109"
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CDS complement(119050..1199 /locus-tag="y0109"
 73)
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CDS 120608..121261
 /note="IS and transposon
 related functions"
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 related functions"
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 putative transposase [Yersinia
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CDS 121258..122040
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 related functions"
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 260 of 260 are 100.00 pct"

identical to residues 1 to 260 of
260 from GenPept : >gb|AAC69770.1|
(AF074612) putative transposase
[Yersinia pestis]"
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residues 35 to 327 of 328 from E.
coli K12 : B3102"
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gene complement(123122..1240 /locus-tag="y0113"
CDS 15)
complement(123122..1240 /locus-tag="y0113"
CDS 15)
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residues 1 to 294 of 298 from E.
coli K12 : B3105"
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SEALSPAWKLFLPIDKLALKANTQVSILTEVLAG

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 VKYRGIAVADTARERPVITVQLLD
 KQQLTVSTIEDKRRALLAGLGVATMPYEMVEKD
 IAAGRLRVIGPEYSREADIMAWR
 RDSDMGEAKSWCLREIPKLLGK"
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CDS complement (124135..1242 /locus-tag="y0114"
 84)
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 residues 1 to 233 of 233 from *E.*
 coli K12 : B3106; residues 1 to
 234 of 234 are 71.79 pct identical
 to residues 1 to 233 of 233 from
 GenPept : >emb|CADD07760.1|
 (AL627278) conserved hypothetical
 protein [*Salmonella enterica*
 subsp. *enterica* serovar *Typhi*]"
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 LGNHVHAKTGDAALLFSPQQGVSY5
 EHNLSSANKSLTRIQLWLNAACPERESA
 PTQHQQLRS
 TRPVQLLASPAGEQGSQSLQRQQM
 IHHHLALAAGEQQKMLPHGHRAYLQS
 IHHGTVDATG
 PQTGTSQRLLTCGGAFVEEEQHLV
 IKAITPLRALLIDLPV"
gene complement (125522..1258 /locus-tag="ys001"
 98)
misc-RNA complement (125522..1258 /locus-tag="ys001"
 98)
 /product="RNase P, RNA component"
 /note="M1 RNA; processes tRNA"
 /function="RNA; Macromolecule
 degradation: Degradation of RNA"
 /locus-tag="y0116"
 /locus-tag="y0116"
 /note="residues 82 to 114 of 122
 are 48.48 pct identical to
 residues 47 to 79 of 271 from
 GenPept : >dbj|BAB31852.1|
 (AK019785) data source:SPTR,
 source key:Q9NQV8, evidence:ISS
 homolog to PR-domain containing
 protein 8 putative [*Mus musculus*]"
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GLSSPPVPSPERDGSEAATV"
gene complement(125918..1268 /locus-tag="y0117"
17)
CDS complement(125918..1268 /locus-tag="y0117"
17)
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residues 1 to 285 of 286 from E.
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DTRHTGILLQHFAINARLFALHDNEQQKADQLL
AKLQEGQSIALVSDAGTPLINDPG
YHLVRCRCAEAGIRVVFLPGACAAITALSAGLAS
DRFCYEGFLPAKTKGRKDILQALI
EEPRTLIFYESTHRLLESLQDMVTVLGPQRYYVVL
ARELTKTWESIHGAPVGELLAWSVK
EEETRRGEMLVIVEGHKVQSDDALPADALRTLAL
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/locus-tag="y0118"
/note="residues 33 to 689 of 689
are 53.00 pct identical to
residues 1 to 678 of 678 from E.
coli K12 : B3147; residues 33 to
687 of 689 are 55.99 pct identical
to residues 1 to 678 of 680 from
GenPept : >gb|AAL22136.1|
(AE008850) paral putative
transglycosylase [Salmonella
typhimurium LT2]"
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SDYYLQQLQQLSSDDNKADWQLLAI
RALLREAKVPQAAEQLSTLPANLSDTQRQEQQLL
AAELLIQAKNTPAAADILAKLEAT
OLSANOKVRYYYAQIAANQDKATLPLIRAFIAQE
PLLTDAKAHQDNIDGTWQSLSQLTP
QELNTMVINADEVNLQGWLDDLRLVYQDNQKDPEL
LKAGIKDWQTRYQPQNPAAKNLPTA
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GFTAAQNGSAVTASVPTPNVTES

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MPLLVLVPGALERIAKAFADEWOKQGGQTVLQQ
NFGSTTELKQSINSGAGIRLTGTP
VSVSNVAAAPASVTIAGLTIPAPPIDAVVSTSS
SGNIDAVIIIAATPSELTLIKPMID
MATSSRSKPALFASSRSYQAGAGPDYRLEMEGIQ
FSDIPLMAGSNPALLOQASAKYAN
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gene 128937..129290
CDS 128937..129290
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/note="residues 1 to 115 of 117
are 57.39 pct identical to
residues 14 to 128 of 131 from E.
coli K12 : B3148; residues 1 to
115 of 117 are 57.39 pct identical
to residues 14 to 128 of 131 from
GenPept : >gb|AAL22137.1|
(AE008850) putative endonuclease
[Salmonella typhimurium LT2]"
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/db-xref="GI:21956784"
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DAWWFVEVRFRNLDLFGGAAASITPRKQQQLHLA
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TGNQLEWLPNAFNTD"

gene complement(129011..1293 /locus-tag="y0120"
91)
CDS complement(129011..1293 /locus-tag="y0120"
91)
/note="residues 3 to 49 of 126 are
37.99 pct identical to residues
674 to 722 of 1684 from GenPept :
>gb|AAC27151.1|AAC27151 (AC004512)
Similar to qb|U46691 putative
chromatin structure regulator
(SUPT6H) from Homo sapiens. ESTs
gb|T42908, gb|AA586170 and
gb|AA395125 come from this gene.
[Arabidopsis thaliana]"
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/db-xref="GI:21956785"
/translation="MLFKLVPDQFFSRLPSACNS
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SNWLVPVIATTSKRQDVVAKLAPRCASQTAARCRS
RCCLRGVILAAAPPNRNSLRRKRTS
TNTHASPSSIIRSISPPRKATLAA"

gene complement(129415..1295 /locus-tag="y0121"
01)
CDS complement(129415..1295 /locus-tag="y0121"
01)
/note="residues 2 to 25 of 28 are

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|------|--------------------------|--|
| | | 50.00 pct identical to residues
839 to 862 of 1165 from GenPept :
>gb AAD10500.2 (U53471) receptor
tyrosine kinase proto-oncogene
[Xiphophorus xiphidium]"
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>translation="MVTLLNPNHLLVVDKFVSKL
IGINEPY" |
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residues 1 to 196 of 196 from E.
coli K12 : B3149"
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LNADNVLTAITNDRLHDEVYAKQ
VRALCQAGDVLLAISTRGRNSRDLVKAVEAAVTRD
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ND" |
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residues 1 to 196 of 196 from E.
coli K12 : B3149"
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LNADNVLTAITNDRLHDEVYAKQ
VRALCQAGDVLLAISTRGRNSRDLVKAVEAAVTRD
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ND" |
| gene | 130117..130737 | /locus-tag="y0123"
>note="residues 16 to 206 of 206
are 73.29 pct identical to
residues 1 to 191 of 191 from E.
coli K12 : B3150; residues 16 to
206 of 206 are 73.82 pct identical
to residues 1 to 191 of 191 from
GenPept : >gb AAL22139.1
(AE008850) paral putative
periplasmic protein [Salmonella
typhimurium LT2]"
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exported protein"
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IKSQTFRVVTAYQGKVLLTGQTPS
AELSNSRAKQIASGVGVTEVYNEMRLGKPVLST
ASMDTWITTKVRSQLLTSDSVKSS
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VKHVTTAFTIVK" |
| CDS | 130117..130737 | /locus-tag="y0123"
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are 73.29 pct identical to
residues 1 to 191 of 191 from E.
coli K12 : B3150; residues 16 to
206 of 206 are 73.82 pct identical
to residues 1 to 191 of 191 from
GenPept : >gb AAL22139.1
(AE008850) paral putative
periplasmic protein [Salmonella
typhimurium LT2]"
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exported protein"
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IKSQTFRVVTAYQGKVLLTGQTPS
AELSNSRAKQIASGVGVTEVYNEMRLGKPVLST
ASMDTWITTKVRSQLLTSDSVKSS
NVKVITENGEVFLLGLVTQQEAQSAQIASKVSG
VKHVTTAFTIVK" |
| gene | complement (130944..1316 | /gene="mtgA"
69) |
| CDS | complement (130944..1316 | /gene="mtgA" |

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/locus-tag="y0124"
/note="residues 17 to 241 of 241
are 72.44 pct identical to
residues 18 to 242 of 242 from E.
coli K12 : B3208"
/codon-start=1
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enzyme"
/protein-id="AAM83718.1"
/db-xref="GI:21956789"
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VMAAEQDKFPDHWGFDVGAIESAL
SHNQRNQKRIRGASTLSQQTAKNVFLWDGRSWR
KGLEVGLTAGIELIWTKRRILTVY
LNIAEFGNGIFGVVEAARRHFFNPKASKLASEAA
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QQWLIRQMHQLGKTFLQENTLD"
gene complement(131666..1323 /locus-tag="y0125"
19)
CDS complement(131666..1323 /locus-tag="y0125"
19)
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are 63.59 pct identical to
residues 4 to 220 of 220 from E.
coli K12 : B3209; residues 1 to
217 of 217 are 65.89 pct identical
to residues 1 to 217 of 217 from
GenPept : >emb|CAD07844.1|
(AL627278) conserved hypothetical
protein [Salmonella enterica
subsp. enterica serovar Typhi]"
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gene complement(132561..1348 /gene="arcB"
97)
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CDS complement(132561..1348 /gene="arcB"
97)
    /locus-tag="y0126"
    /function="enzyme; global
regulatory functions"
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to 778 of 778 are 75.92 pct
identical to residues 1 to 776 of
776 from E. coli K12 : B3210;

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residues 1 to 778 of 778 are 77.33
 pct identical to residues 1 to 778
 of 778 from GenPept :
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 histidine kinase in two-component
 regulatory system with ArcA,
 senses redox conditions
 [Salmonella typhimurium LT2]"
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 sensor-response protein; histidine
 protein kinase/phosphatase"
 /protein-id="AAM83/20.1"
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 ELNKQLTENITQLNQEIVEREKAELKAHQVVDKL
 KEEMGHREQAQIELGQQQSALLRSF
 LDASPDLYYRNEDENEFGCNRAMELLTGKSEQ
 LVGLTPKDVKYAPDIAEKVVMETDEK
 VFRHNVSILTYEOWLVPDGRKACFELRKVPFYDR
 VGKRHGLMGFRGDITERKRYQDAL
 ENASRDKTTFISTISHELRTPNLNGIVGLSRILLD
 TELDAEQLKYLKTIHVSAILGNI
 FNDI1EMDKLERRKVQOLDNQPVDFGMADLENL
 SGLLVQPQKGLKFIMEPQLPLPEKV
 IADGTRLRLQILWNLIGNAVKFTQQGKIVVRVRE
 GNDRLIFEVEDSGMGIPEDEQDKI
 FAMYQQVDRNGGRPATGTGIGLAVSKRLAQSMG
 GDITVKSTQGVGSCFTLTIKAPAV
 QEASNAFSGDDMPFLPALHVLLVEDIELNVIVARS
 VLEKLGNNSVDAVMNGHDALAMFNP
 EDFDLVLLDIQLPDMSGLDIARQIRAEYGKQSLP
 PLVALTANVLKDKKEYLDAAGMDDV
 LSKPLSVPALTAMIKQFWDSKPSSAVQKQEHKVM
 QTHESLDDTTMLEQYIDLVGPQLI
 HQSLEMFEQMMPGYLAVLDSNMTARDQKGITEEA
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 VEKK"

| | |
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| | 50) |
| CDS | complement (135161..1361 /locus-tag="y0127" |
| | 50) |
| | /note="residues 23 to 323 of 329
are 78.73 pct identical to
residues 1 to 301 of 309 from E.
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LAYFOQAYTSTYAEVNALAAAMYQQALCEADIVGLC
VGTRPDCVFDALDLSYQQQGY" |

EVWLELGLQTANDKTLKRINRGHDFACYQQTARR
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 RETLEKVVITGVVDGIKLHFLHIVEGSTMAKAWRA
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 gene 136757..141364
 CDS 136757..141364
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 /locus-tag="y0128"
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 /function="enzyme; central
 intermediary metabolism: Pool,
 multipurpose conversions"
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 residues 24 to 1517 of 1517 from
 E. coli K12 : B3212; residues 51
 to 1535 of 1535 are 89.23 pct
 identical to residues 1 to 1486 of
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 glutamate synthase large subunit
 [Klebsiella aerogenes]"
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 large subunit"
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 VRTAIHALARMQH RGA ILADGKTG
 DGC GLLL QKPDHF HFRMVVAE ERGWR LAKN YAVGMM
 FLSQDEELAKASRR IVEEE LQNET
 LSIVGWREVP TNP DVLG EIALSSL PR IEQ IF VN
 PAGWRSR DMERR LFV ARR I EKRI
 SDKD FYAC SFN LVTI YK GLC MPAD LPR FYLD LA
 DLR LES AICLF H QRF STNT VP RW P
 LAQP FRYLAH NG EINTI AGNR QWA KARAY KFK TP
 LIPDLQDA APF VNET GS DSS LDN
 MLELF LSG GMOL IRAM RLL VP PAW QNNP DMD TD
 RAFFDFN SMH MHEP WD CGP AIV VMSD
 GRYAAC NLD RNL G LR PARY VIT KDKL IT CASE VG
 WD YQ DVE VKE GRV GP GEL MVIDT
 RSGKILH SAET ND LKS RHP YKE WME KNV KR LVP
 FED LPEE QVG S RQ LD S SO LET YK
 QFG YNS NEELD QI I RV L GENG QEA TGS MG DD TPF A
 VLSSGP RI YYD YF RQ QFA QV TN P
 IDPL REAH VMS LATS I G R E MN VF C EA EG QA HRL S
 FKSP ILL Y SDF QQL TT LE GE HY RA
 DRLL DTF NP AEND L QEA V L SLC DEA E R K V RD GAV
 M L V L S D R IA P N RL VP APM AV GA
 I QTR L V D KSL RCD A NI I V ET A SARD P H FA V LL G
 FGATA I YP LAY E SLAK L V D SQ A I
 DKK YRD VM NY RNG IN K GLY K I M SK MG I ST V AS Y
 R C A K L F E A V G L H R D L S D L C F Q G V V
 SRIGGASFSDF Q QD L QN L S K R A W L K R K P L D Q G G L
 LKF V H N G E Y H A Y N P D V U S T L Q K A V
 HSG E YSD V Q A Y A K L V N E P R I A T L R D L L A I K P Q G T
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 G A L S P E A H E S L A I M N S L G G F S N S G E G G E D P A R Y

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 KTGVDIVKAAILGAESFGFTGPM
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 LPERVNVYHFPIARETREIMAEGL
 VSQVLVDLIGRTDMLELDGDISAKQNKLDSLSPMLK
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 NKELLSQAEPYIEAKQSCTFYFDIRNTDRSGVAA
 LSGAIATKHGDQGLATDPPIKEYS
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 RIAVRPPVGSNFRSHEASIIGNTC
 LYGATGGKLFAAGRAGERFAVRNSGAITVVEGIG
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intermediary metabolism: Pool,
multipurpose conversions"
/note="residues 1 to 472 of 472
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residues 1 to 472 of 472 from E.
coli K12 : B3213; residues 1 to
472 of 472 are 84.74 pct identical
to residues 1 to 472 of 472 from
GenPept : >gb|AAK94788.1|
(AY035435) glutamate synthase
small subunit [Klebsiella
aerogenes]"
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small subunit"
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 PDMSHVHTGKRAVIGAGPAGLA
 CADVLARNGVQAVVFDRHPFEGGLLTFGIPAFKL
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 EANGVYDALPFLIANTKQLMGYEA
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 LGAPDAQGRRMAEQIPGSEHVLPA
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 CDS 141374..142792
 gene 143233..143718

CDS 143233..143718 /locus-tag="y0130"
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residues 2690 to 2740 of 3744 from
GenPept : >gb|AAB68923.1| (U00060)
Tralp [Saccharomyces cerevisiae]"
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gene complement(143871..1443 /gene="sspB"
86) /locus-tag="y0131"
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86) /locus-tag="y0131"
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residues 1 to 165 of 165 from E.
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protein B"
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SGGRPALRVVK"
gene complement(144392..1450 /gene="sspA"
33) /locus-tag="y0132"
CDS complement(144392..1450 /gene="sspA"
33) /locus-tag="y0132"
/function="regulator; global
regulatory functions"
/note="residues 1 to 209 of 213
are 83.73 pct identical to
residues 1 to 209 of 212 from E.
coli K12 : B3229; residues 1 to
213 of 213 are 100.00 pct
identical to residues 1 to 213 of
213 from GenPept :
>emb|CAC92790.1| (AJ414157)
putative stringent starvation
protein A [Yersinia pestis]"
/codon-start=1
/transl-table=11

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FSHQVRIVLAEKGVSVEIEQVEAD
NLPQDLIDLNPYRTVFTLVDRELTLYESRIIMEY
LDERFPHPFLMPVYPVARGSSRLM
MHRIEHDWYSLLYKIEQGNAQEEAARKQLREEL
LSIAFPVNETPFFMSEEFSLVDCY
LAPLLWRLPVLGIEFTGAGSKELKGYMTRVFERD
AFLASLTEAEREMHLKTRS"
gene complement(145407..1458 /gene="rpsI"
05)
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CDS complement(145407..1458 /gene="rpsI"
05)
/locus-tag="y0133"
/function="structural component;
ribosomal proteins - synthesis,
modification"
/note="residues 3 to 132 of 132
are 92.30 pct identical to
residues 1 to 130 of 130 from E.
coli K12 : B3230; residues 3 to
132 of 132 are 93.07 pct identical
to residues 1 to 130 of 130 from
GenPept : >gb|AAL22213.1|
(AE008854) 30S ribosomal subunit
protein S9 [Salmonella typhimurium
LT2]"
/codon-start=1
/transl-table=11
/product="30S ribosomal subunit
protein S9"
/protein-id="AAM83727.1"
/db-xref="GI:21956800"
/translation="MAMAENQYYGTGRRKSSAR
VFLKPGSGKIVINQRSLEVYFGRE
TARMVNQPLELVDMVTKFDMYITVKGGGISGQA
GAIRHGITALMEYDESLRGELRK
AGFVTRDAREVERKKVGLRKARRRPQFSKR"
gene complement(145814..1462 /gene="rplM"
57)
/locus-tag="y0134"
CDS complement(145814..1462 /gene="rplM"
57)
/locus-tag="y0134"
/function="structural component;
ribosomal proteins - synthesis,
modification"
/note="residues 6 to 147 of 147
are 95.07 pct identical to
residues 1 to 142 of 142 from E.
coli K12 : B3231"
/codon-start=1
/transl-table=11
/product="50S ribosomal subunit
protein L13"
/protein-id="AAM83728.1"
/db-xref="GI:21956801"

/translation="MGKLLMKTFTAKPETVKRDW
YVVDASGKTLGRILATELARRLRKG
HKAETYTHVDTGDYIIVLNAEKVAVTGNKRTDKI
YYHHTGFVGGIKQATFEMIARRP
ERVIEIAVKGMLPKGPLGRAMYRKLVYAGTEHN
HAAQQPQLDI"
gene complement (146556..1476 /locus-tag="y0135"
95)
CDS complement (146556..1476 /locus-tag="y0135"
95)
/note="residues 5 to 378 of 379
are 64.97 pct identical to
residues 1 to 373 of 379 from E.
coli K12 : B3232; residues 5 to
379 of 379 are 66.66 pct identical
to residues 1 to 374 of 374 from
GenPept : >gb|AAL22215.1|
(AE008854) putative ATPase
[Salmonella typhimurium LT2]"
/codon-start=1
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/db-xref="GI:21956802"
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GGYQFDVQRRAVARLETTIYQALN
QYQNVPAAASASLRNRLGRGLFGKPARPPVSPVQG
LYMWGVGRGKWTLMDFLFFHSLEG
ERKLRLHFHRFMLRVHQELTELQGHENPLEIVADL
GFKAQTDVLCFDEFFVSDITDAML
LATLLEALFARGITLVATSNIIPPNDLYHNGLQRG
RFLPAIALIKQHCEVMNVDAgidY
RLRILTQANLYLTPLNSQTEQAMAIFVVKLAGKE
GGKATLEVNHRLPAICVAEGVL
AVDFHTLCEEARSQLDYIALSKRYHTVLLHNVR
MAARDENTARRFLALVDEFYERRV
KLIIAAEASMFEIYSGERLKFEYQRCLSLRQEMQ
SEEYLSQLPHLP"
/locus-tag="y0136"
/locus-tag="y0136"
/note="residues 1 to 127 of 134
are 80.31 pct identical to
residues 3 to 128 of 134 from E.
coli K12 : B3233; residues 1 to
127 of 134 are 80.31 pct identical
to residues 3 to 128 of 134 from
GenPept : >gb|AAL22216.1|
(AE008854) putative periplasmic
protein [Salmonella typhimurium
LT2]"
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/protein-id="AAM83730.1"
/db-xref="GI:21956803"
/translation="MTWEYALIGLVVGVVIGAVA
MRFGNRKLROQQVLONELEKSKD
LEEYRQEVLVGHFARSAAELDNMARDYRQLYQHMA
KSSNLLLPDLPLQDNFPRYRLTES
EADNDQAPVKLPRDYSEGASGLLRPEHQNRD"
/gene="degQ"
/locus-tag="y0137"
gene 147907..148311
CDS 147907..148311
gene 148564..149955

CDS 148564..149955 /gene="degQ"
/locus-tag="y0137"
/function="enzyme; degradation of
proteins, peptides, glyco"
/note="residues 7 to 463 of 463
are 72.05 pct identical to
residues 1 to 455 of 455 from E.
coli K12 : B3234; residues 7 to
463 of 463 are 72.92 pct identical
to residues 1 to 455 of 455 from
GenPept : >gb|AAL22217.1|
(AE008854) serine endoprotease
[Salmonella typhimurium LT2]"
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/transl-table=11
/product="serine endoprotease"
/protein-id="AAM83731.1"
/db-xref="GI:21956804"
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VGLGLASVPMVSAALPAAVAGOT
LPSLAPMLEKVLPVVSVHVGSGQAQQQLPEEF
KFFFGPNAPSGKESSRPFEGLGSG
VIINAEGYIILTNNHVINNADKIRVQLNDGREYD
AKLLGRDEQTDTIALQLTDAKNLT
AIKIAKSDNLRVGFDFAVAVGNPFLGQTATGII
SALGRSGLNLEGLENFIQTDASIN
RGNSGGALVNLDGELIGINTAILAPGGGNIGIFG
AIPSNMAQNLSQQLIEFGEVKRGL
LGIRGSEMTADIAKAFNIDAQORGAFVSEVLPKSA
AAKAGIKPGDVLIISVDGKKISSFA
ELRAKVGTTGGKTIKIGLRLREGKPLEVSVTLDN
SSSTSTSAENLSPSLOGASLSNGE
LKDGSKGIKVDSVTGPSAAQSGLQKDDVIIAVN
RERVKDIAELRAKIAEKAPEAVIALN
IVRGEDNITYLLIR"
repeat-region complement(149966..1506 /note="insertion element"
75)
/insertion-seq="IS1541a"
gene complement(150072..1505 /locus-tag="y0138"
81)
CDS complement(150072..1505 /locus-tag="y0138"
81)
/function="IS and transposon
related functions"
/note="IS1541a; residues 1 to 169
of 169 are 99.40 pct identical to
residues 1 to 169 of 169 from
GenPept : >gb|AAC82673.1|
(AF074611) transposase [Yersinia
pestis]"
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/transl-table=11
/product="putative transposase"
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/db-xref="GI:21956805"
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EKSLAHTRWNCKYHIVFAPKYRRO
VFYREKARRAIGSILRKLCWEKVNILEAECCVDH
IHMLLEIPPKMSVSGFMGYLKGS
SLMLYEQFGDLKFKYRNREFWCRGYYVDTVGKNT
ARIQEYIKHQLEEDKMGEQLSIPY
PGSPFTGRK"

| | | |
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| gene | 150756..151844 | /gene="degS"
/locus-tag="y0139" |
| CDS | 150756..151844 | /gene="degS"
/locus-tag="y0139"
/function="enzyme; degradation of
proteins, peptides, glyco"
/note="residues 1 to 349 of 362
are 71.22 pct identical to
residues 1 to 350 of 355 from E.
coli K12 : B3235"
/codon-start=1
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/product="protease"
/protein-id="AAM83733.1"
/db-xref="GI:21956806"
/translation="MFLKLRLSIIILGLIVAGILL
VALPMLRSPLSPGVLFSGKSSNNVNEEV
PTSYNQAVRRAAPAVNVNVRSLSATQQGLAIRT
LGSGVIMSDKGYIILTNKHVINDAE
QIIVAMQNGRISEALLVGSDNLTDLAVLKIDATN
LPVIPININRTPHIGDVVLALIGNP
YNLQGTVTQGIISATGRIGLSSSGRNQFLQTDAS
INQGNSSGGALVNLTGELMGINTL
FDKSNNGNGETPEGIGFAIPTALATKVMKEKLIRDGR
VIRGYIGITGEYEPFPFNANDNGSD
RVHGIKVKKVSPDGPAAQAGIHVGDIILNVNNKP
ATSVIETMDQVAEVVRPGTTIPVLL
LRNGQQIAVQITITELDQNEMLTTQAAD" |
| gene | complement (152025..1532
87) | /gene="murA"
/locus-tag="y0140" |
| CDS | complement (152025..1532
87) | /gene="murA"
/locus-tag="y0140"
/function="enzyme; murein
sacculus, peptidoglycan"
/note="first step in murein
biosynthesis; residues 1 to 420 of
420 are 88.80 pct identical to
residues 1 to 419 of 419 from E.
coli K12 : B3189; residues 1 to
420 of 420 are 100.00 pct
identical to residues 1 to 420 of
420 from GenPept :
>emb CAC92798.1 (AJ414157)
UDP-N-acetylglucosamine
1-carboxyvinyltransferase
[Yersinia pestis]"
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1-carboxyvinyltransferase"
/protein-id="AAM83734.1"
/db-xref="GI:21956807"
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PKLKDIDTTIKLLSOLGTKLERNNGSVFDASAV
NEFCAPYDLVKTMRASIWAQGPLV
ARFGQQGVSLPGGCAIGARPVDLHITGLEQLGAE
IKLEEGYYVKASVNGLRGKAHVMD
KVSVGATVTIMSAATLAEGTTVIENAAREPEIVD
TANFLNTLGAKISGAGTDRITIEG" |

VTRLGGGVYRVLPDFRIETGTFLVAAAISGGKVV
RQTRPDTLDAVLAKLREAGADIEV
GDDWISLDMKGKRPKAITFRTAPHGPFTDMQAQ
FSLLNLVAEGTGVITETIFENRFM
HVPFLIRMGAHAEIESNTVICYGVQLSGAQVM
TDLRASASLVLAGCIAEGVTIVDR
IYHIDRGRYERIEDKLRALGAKIERVKGE"

gene complement (153441..1537 /locus-tag="y0141"
04)
complement (153441..1537 /locus-tag="y0141"
04)
/note="residues 4 to 87 of 87 are
80.95 pct identical to residues 6
to 89 of 89 from E. coli K12 :
B3190; residues 4 to 87 of 87 are
80.95 pct identical to residues 6
to 89 of 89 from GenPept :
>gb|AAG58324.1|AE005547-10
(AE005547) orf, hypothetical
protein [Escherichia coli O157:H7
EDL933]"
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/db-xref="GI:21956808"
/translation="MNLMDTNEIKDVLMLNALQ
EAHVITGDGSFHQIVVVGELFADMN
RVKKQOAVYAPLMEYIADNRHLSIKAYTPQEW
QRDRKLNGF"
gene complement (153842..1541 /locus-tag="y0142"
44)
complement (153842..1541 /locus-tag="y0142"
44)
/note="residues 1 to 90 of 100 are
43.33 pct identical to residues 33
to 122 of 129 from E. coli K12 :
B3191; residues 1 to 90 of 100 are
43.33 pct identical to residues 33
to 122 of 129 from GenPept :
>gb|AAG58325.1|AE005547-11
(AE005547) yrbB gene product
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83736.1"
/db-xref="GI:21956809"
/translation="MAGELSWQSLQETLVLQGEL
DRETILLPLWQQRETILLADKSRIDV
SQLQRVDSSGLALLVHFRELQSQRGHSLLEIGIS
NRLATLIELYNLQQIIPVETAS"
gene complement (154180..1548 /locus-tag="y0143"
03)
complement (154180..1548 /locus-tag="y0143"
03)
/note="residues 1 to 207 of 207
are 77.51 pct identical to
residues 1 to 209 of 211 from E.
coli K12 : B3192; residues 1 to
207 of 207 are 77.51 pct identical
to residues 1 to 209 of 211 from

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GenPept : >gb|AAL22179.1|
(AE008852) putative ABC
superfamily (atp and memb),
transport protein [Salmonella
typhimurium LT2]"
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/protein-id="AAM83737.1"
/db-xref="GI:21956810"
/translation="MFKRLFMVALLAIAPLVHAV
DQSNPYRLMDEAAKKTFTRLKNBQ
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YYKDATPAQREAYFNAFGKYLEQA
YGQALALYHGQTYDVAPDQPLGDANIVAIRVTIL
DPSGRPPVRLDFQWRKNNSQTGNWQ
AYDMIAEGVSMISTKQNNEWASILRQKGVGDLTQQ
LLSAAKQPITLDK"

gene complement(154816..1553 /locus-tag="y0144"
88)
CDS complement(154816..1553 /locus-tag="y0144"
88)
/NOTE="residues 6 to 178 of 190
are 71.67 pct identical to
residues 1 to 170 of 183 from E.
coli K12 : B3193; residues 6 to
184 of 190 are 67.59 pct identical
to residues 1 to 179 of 183 from
GenPept : >gb|AAL22180.1|
(AE008852) putative ABC
superfamily (bind-prot) transport
protein [Salmonella typhimurium
LT2]"
/codon-start=1
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/product="hypothetical protein"
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/db-xref="GI:21956811"
/translation="MGTESMQTKSEWWGMFIL
IAILAVIFLCLKVADIKSVGNQPT
YRIYANFDNIGGLKNHSPVKIGGVVVGRVAEITL
DTKNYTPRAIDIQQRYNHIPDTS
SLAVRTSGLLGEQFLALNVGFEDPEMGTSILKDG
GTIQDTKSALVLEDLIGQFLYKSS
GDSPFAVESETAPATEAAPQAAVPSLPAQHP"

gene complement(155378..1561 /locus-tag="y0145"
60)
CDS complement(155378..1561 /locus-tag="y0145"
60)
/NOTE="residues 1 to 260 of 260
are 82.69 pct identical to
residues 1 to 260 of 260 from E.
coli K12 : B3194"
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/transl-table=11
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/protein-id="AAM83739.1"
/db-xref="GI:21956812"
/translation="MLVKSLASLGRRGINVCASF
GRAGLMLFNALVGRPEPRKQWPPLL
IKQLYSVGVQSSLIIIVVSGFIGMVGLQGFLIL
TTYSAEASLGMMVSLSLRELGPV

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VTALLFAGRAGSALTAEIGLMKATEQISSLEMA
 IDPLRRVVAAPRFWAGLISMLPLTA
 IFVAVGIGGGSVVGVDWKGIDSQGFWSAMQNAVE
 WRTDLLNCLIKSLVFALTVTWIAL
 FNGYDAVPITSEGISRATTRTVVHSSLAVLGLDFV
 LTALMFGN"
gene complement (156378..1571 /locus-tag="y0146"
 96)
CDS complement (156378..1571 /locus-tag="y0146"
 96)
 /feature="protein"
 /function="putative transport"
 /note="residues 4 to 269 of 272
 are 78.19 pct identical to
 residues 1 to 266 of 269 from E.
 coli K12 : B3195"
 /codon-start=1
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 /product="putative ATP-binding
 component of ABC transport system"
 /protein-id="AAM83740.1"
 /db-xref="GI:21956814"
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 RGERLIFADINMTVPRGVTAIMG
 PSGIGKTTLRLIGGOLAPDTGEIWFDDGNIPAL
 SRQRLYDVRKKMSMLFQSGALFTD
 LTVFENVAFPLREHSRRLPEELLNSTVMMKLEAVG
 LRGAANILMPAELSGGMARRAALAR
 AIALDPELIMFDEPFVQGDPITMGVLVKLIDELN
 HALGVTCVVVSNDVPEVLSIADYA
 YIVADQHVNIAEGTPEQLOQTNSDMRVRQFLDGIAD
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gene 157461..158435 /locus-tag="y0147"
CDS 157461..158435 /locus-tag="y0147"
 /feature="protein"
 /note="residues 1 to 318 of 324
 are 60.69 pct identical to
 residues 1 to 318 of 325 from E.
 coli K12 : B3196; residues 1 to
 318 of 324 are 63.52 pct identical
 to residues 1 to 318 of 325 from
 GenPept : >emb|CAD07831.1|
 (AL627278) putative membrane
 protein [Salmonella enterica
 subsp. enterica serovar Typhi]"
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 RLVYGAAVLRSRSEGVFPPLIIGMTI
 VGIGTSLPELIVSVAALNQTDMAVGNVLGSNI
 TNLLLIVGGAALIRPLIVRSEILR
 RELPLMLVVTTALCGFLLAQNHLSRGGVGIVLLAA
 AAFIVLMLKIAIRLAHEEGNDILTR
 EQLSELPQDSSTTVALLWLVLAIFIILPLSAKII
 DNATVAVGAVSELVIGLTIVIA
 GTSLPELATFIAGALKGENDIAVGNIIIGSNFNI
 VIVLGVPALLSPGEINPEAFQRDY
 WVMLAVSVVFTLLCLGRKRHRIGHLAGALLCGFI
 TYLAFLVFFAPISAL"
gene 158459..159532 /locus-tag="y0149"
CDS 158459..159532 /locus-tag="y0149"

/note="residues 30 to 357 of 357
 are 77.43 pct identical to
 residues 1 to 328 of 328 from E.
 coli K12 : B3197; residues 30 to
 357 of 357 are 78.65 pct identical
 to residues 1 to 328 of 328 from
 GenPept : >gb|AAL22184.1|
 (AE008852) putative polysialic
 acid capsule expression protein
 [Salmonella typhimurium LT2]"
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 /protein-id="AAM83742.1"
 /db-xref="GI:21956816"
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 NTNIGRILSMSTFDLQPGVDFQQA
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 GKVVMGMGKSGHIGCKIAATFAS
 TGTPAFVHPGEASHGDLGMITPQDIVLAISNSG
 ESNEILLTIPVLKRKQILLICMSS
 NPESTMGAADIHLCLINVQPACPLGLAPTTSTT
 ATLVMGDLAVALLKARGFTQEDF
 ALSHPGGALGRKLLRISIDIMHTGTEIPTVSPDA
 SLRDALLEITRKSGLLTVICDDSM
 RIKGIFTDGDLRVRFDMGIDLNNAKIAIDVMTRGG
 IRVPPNLAVDALNLMESRHITAL
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 gene complement(159121..1594 /locus-tag="y0148"
 08)
 CDS complement(159121..1594 /locus-tag="y0148"
 08)
 /note="residues 18 to 78 of 95 are
 32.78 pct identical to residues
 645 to 704 of 918 from GenPept :
 >gb|AAA33114.1| (M33154) nitrate
 reductase [Cucurbita maxima]"
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 /product="hypothetical"
 /protein-id="AAM83743.1"
 /db-xref="GI:21956817"
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 SQITVKPRFLRVISSKASRNDAASGLTVGIVSPVC
 IIISLRSSNLRPSAPFG"
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 CDS 159781..160344 /locus-tag="y0150"
 /note="residues 5 to 187 of 187
 are 77.04 pct identical to
 residues 6 to 188 of 188 from E.
 coli K12 : B3198"
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 RAANIRLLICDVGVMPSDGLIYMG
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 AKLLEDRAANTLGITHLYQQGSDKL
 VAYHELLATLQCQEPAVYIGDDLIDWPVMAQVG"

LSVAVADAHPLLPAHYVTRIG
GRGAVRECDLILLAQDKLEGATGLSI"
gene 160341..160904
CDS 160341..160904

/locus-tag="y0151"
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/note="residues 1 to 186 of 187
are 55.91 pct identical to
residues 1 to 185 of 191 from E.
coli K12 : B3199"
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FTKPVMTLFGDNAAVATWTVRADRA
KLTDDKMLYLYGHVEVDSDLTADAQLKKIRTDNAQ
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/note="residues 8 to 177 of 188
are 69.76 pct identical to
residues 1 to 172 of 185 from E.
coli K12 : B3200; residues 8 to
187 of 188 are 69.94 pct identical
to residues 1 to 183 of 184 from
GenPept : >gb|AAL22187.1|
(AE008852) putative ABC
superfamily (bind-prot) transport
protein [Salmonella typhimurium
LT2]"
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/db-xref="GI:21956820"
/translation="MKRLKPLMKSKNKISHLLA
CSLLAASLSAFALTGDTEQFPAEVK
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VTRPGGDQSMMIEFGFNPVTFYQ
MQDSGKPVKGHQQKLRYEIANDFVVLTGDAYLEQ
LDSNIKGDRITYLVKKQQMEAIFSD
KGKRTTVLFLPSQLQDKGPAAAGQKKSK"
/locus-tag="y0153"
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/function="putative transport"
/note="residues 1 to 241 of 241
are 88.79 pct identical to
residues 1 to 241 of 241 from E.
coli K12 : B3201; residues 1 to
241 of 241 are 88.79 pct identical
to residues 1 to 241 of 241 from
GenPept : >gb|AAL22188.1|
(AE008852) putative ABC
superfamily (atp-bind) transport
protein [Salmonella typhimurium
LT2]"
/codon-start=1
/transl-table=11
/product="putative ATP-binding

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| | | component of ABC transport system" |
| | | /protein-id="AAM83747.1" |
| | | /db-xref="GI:21956821" |
| | | /translation="MATLIAEKLAKAYKGRKVVE |
| | | DVSLNVKSGEIVGLLGPNGAGKT |
| | | TFYMGVGIVQRDAGRIVIDDEDISLLPLHERARR |
| | | GIGYLHQEASIFRRLSVFNNLMAV |
| | | LEIRKDLSAEQREERAEELMEEFHINHLRDSLQG |
| | | SLSGGERRRVEATARALAANPKFIL |
| | | LDEFFAGVDPISVIDIKKIIKHLRDGLGVLIID |
| | | HNVRETLDVCERAYIVSQGHLIAH |
| | | GTPQDILADEQVKRVYLGEFFRL" |
| gene | 162227..163660 | /gene="rpoN" |
| CDS | 162227..163660 | /locus-tag="y0154" |
| | | /gene="rpoN" |
| | | /locus-tag="y0154" |
| | | /function="regulator; global |
| | | regulatory functions" |
| | | /note="nitrogen and fermentation |
| | | regulation; residues 1 to 477 of |
| | | 477 are 82.59 pct identical to |
| | | residues 1 to 477 of 477 from E. |
| | | coli K12 : B3202; residues 1 to |
| | | 477 of 477 are 82.38 pct identical |
| | | to residues 1 to 477 of 477 from |
| | | GenPept : >emb CAA26925.1 |
| | | (X03147) ntrA protein (aa 1-477) |
| | | [Klebsiella pneumoniae]" |
| | | /codon-start=1 |
| | | /transl-table=11 |
| | | /product="RNA polymerase, sigma(54 |
| | | or 60) factor" |
| | | /protein-id="AAM83748.1" |
| | | /db-xref="GI:21956822" |
| | | /translation="MKQQLQLKFSQQLAMTPQLQ |
| | | QAIRLQLSTLQLQEIQOLALESN |
| | | PLLEQTDLHEEIDAKETVDSESLDTREALEQKDM |
| | | PEELPLDATWDEIYTAGTFSGMGN |
| | | DYSDELPLVQGETTQTLQDYLMWQVQLPFTET |
| | | DAAIATISIVDAVDDTGYLTVPLED |
| | | ILESMDGENVALDEVAVLKRIQHFDPIGHVAARN |
| | | LRECLLVQLSQYAKDTPYLAEARL |
| | | IVSEYLDLGNHDFRMMIRLSRLKEDTLKEAIAL |
| | | IQLSLDPRPGQSINTGESEYVIPDV |
| | | LVRKEKGIVTVELNADSIPLRKVNQQYAAMGNSV |
| | | RNDSDGQFIRSNLQEAWLWIKSLE |
| | | SRNETLILKVARCIVEQQVEFFEKGAEFMCKPMVLA |
| | | DIAQAVDMHESTISRVVTQKFLHS |
| | | PRGIFELKYFFFSSHVNTDSGGEASSTAIRALVKK |
| | | LVAEEENPAKPLSDSKLTTLCEOG |
| | | IMVARRTVAKYRESLSIPPSNQRKQLV" |
| gene | 163684..163791 | /locus-tag="y0155" |
| CDS | 163684..163791 | /locus-tag="y0155" |
| | | /function="putative regulator; |
| | | global regulatory functions" |
| | | /note="residues 1 to 35 of 35 are |
| | | 94.28 pct identical to residues 1 |
| | | to 35 of 95 from GenPept : |
| | | >gb AAL22190.1 (AE008852) |
| | | putative sigma N modulation factor |
| | | [Salmonella typhimurium LT2]" |
| | | /codon-start=1 |

/transl-table=11
/product="putative sigma-54
modulation protein"
/protein-id="AAM83749.1"
/db-xref="GI:21956823"
/translation="MOLNITGHHVITEALREFV
TTKFAKLEQYFDRIN"
/locus-tag="y0156"
/locus-tag="y0156"
/function="putative regulator;
global regulatory functions"
/note="residues 1 to 57 of 57 are
73.68 pct identical to residues 39
to 95 of 95 from *E. coli* K12 :
B3203; residues 1 to 57 of 57 are
77.19 pct identical to residues 39
to 95 of 95 from GenPept :
>emb|CAA34391.1| (X16335) ORF95
peptide (AA 1-95) [Klebsiella
pneumoniae]"
/codon-start=1
/transl-table=11
/product="probable sigma-54
modulation protein"
/protein-id="AAM83750.1"
/db-xref="GI:21956824"
/translation="MVLSEVKVKQIAEATVHVN
GELHASSEQEDMYAAIDILVDKLA
RQLNKHKDKLKQH"
/gene="ptsN"
/locus-tag="y0157"
/gene="ptsN"
/locus-tag="y0157"
/function="enzyme; transport of
small molecules; amino acids,
amines"
/note="regulates N metabolism;
residues 7 to 158 of 164 are 86.18
pct identical to residues 4 to 155
of 163 from *E. coli* K12 : B3204;
residues 7 to 158 of 164 are 86.18
pct identical to residues 4 to 155
of 163 from GenPept :
>gb|AAG58338.1|AE005548-9
(AE005548) phosphotransferase
system enzyme IIA, regulates N
metabolism [Escherichia coli
O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="phosphotransferase
system enzyme IIA"
/protein-id="AAM83751.1"
/db-xref="GI:21956825"
/translation="MKDEMTNDPALQLSSVLNIE
STKSSVHCSSKKRALEIISELAAK
QLNLPSQVVFDAVLTRERMGSTGIGSGIAIPHKG
LEEDTLRAVGVFIRLEQPIAFDAI
DNQPVDLLFALLVPADQCKTHLHTLSVALKRLAD
KTVCRRLRSAQSDDELYQIITELP PEIA"
/locus-tag="y0158"
/locus-tag="y0158"

gene 163798..163971
CDS 163798..163971

gene 164077..164571
CDS 164077..164571

gene 164877..165731
CDS 164877..165731

```

/note="residues 1 to 283 of 284
are 94.34 pct identical to
residues 1 to 283 of 284 from E.
coli K12 : B3205"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83752.1"
/db-xref="GI:21956826"
/translation="MVL MIVSGRSGSGKVALRA
LED MGFYCVNDLPVVL PQLASTL
ADRNISAAVSIDVRNMPESPEVFEHAMTQLPDSF
SPQLLF DADRN T LIRRYS DTRL R
HPLSAKNL SLESAIDE ESDL LEPLRSRADLIIDT
SEMSVHELAEMLRTRLLGKREREL
TMVFESFGFKHGIPIDADYDVFDRVFLPNPHWDPK
LRPMTG LDKPVIS FFLDRHTEVHNFE
IYQTRS YLQE QWLPML ETNNR SYLTVAIGCTGGKH
RSVIVAEQ LADYFR ARGK NVQSRH RT LEKRKQ"
/gene="ptsO"
/locus-tag="y0159"
/gene="ptsO"
/locus-tag="y0159"
/function="transport; transport of
small molecules; Other"
/note="nitrogen related, exchanges
phosphate with Enzyme I, HPr;
residues 1 to 90 of 90 are 87.77
pct identical to residues 1 to 90
of 90 from E. coli K12 : B3206;
residues 1 to 90 of 90 are 85.55
pct identical to residues 1 to 90
of 90 from GenPept :
>gb|AL22193.1| (AE008853) NPr,
phosphocarrier protein HPr-like
NPr, nitrogen related, exchanges
phosphate with Enzyme I
[Salmonella typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="phosphocarrier protein
HPr-like NPr"
/protein-id="AAM83753.1"
/db-xref="GI:21956827"
/translation="MTVKQTVEIKNKLGMHARPA
MKLFELVQSFD AEVMLR ND SGTEA
EASSVIALML DSAKGRQIE VEATGVDEIQ ALAA
VIELFNSGFDED"
/gene="complement(165896..1661"
/locus-tag="y0160"
47)
/complement(165896..1661
/locus-tag="y0160"
47)
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83754.1"
/db-xref="GI:21956828"
/translation="MHVVQQNIGGFSSFPANCG
ELYSLISLQGVKIVFVFLSKRLP
TLR ALP IFLVKSRIKQLDNRCQCLNF INPGCFNL
YAAFG"
/gene="pyrB"

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CDS 166338..167273 /locus-tag="y0161"
/gene="pyrB"
/locus-tag="y0161"
/function="enzyme; pyrimidine
ribonucleotide biosynthesis"
/note="residues 1 to 311 of 311
are 84.88 pct identical to
residues 1 to 311 of 311 from E.
coli K12 : B4245; residues 1 to
311 of 311 are 85.85 pct identical
to residues 1 to 311 of 311 from
GenPept : >gb|AAL23279.1|
(AE008909) aspartate
carbamoyltransferase, catalytic
subunit [Salmonella typhimurium
LT2]"
/codon-start=1
/transl-table=11
/product="aspartate
carbamoyltransferase, catalytic
subunit"
/protein-id="AAM83755.1"
/db-xref="GI:21956830"
/translation="MANPLYHKHIIISINDLSRDE
LELVLRATAASLKKTPPOPELLKHKV
IASCCFFEASTRTRLSFETSIHRLGASVVGFSDDSS
NTSLGKKGETLADTMWSVISTYVDA
IVMRHPQEGASRLAAOFSGNVPIVNAGDGANQHP
TQTLLDLFTIQETQGRLDNINIAM
VGDLKYGRTVHSLTQALAKFNGNHHFFFIAPDALA
MPAYILQMLEEKEIEYESLHESLEE
VVPEDLILYMTRVQKERLDPSEYANVKAQFLRS
SDLTGARDNLKVLHPLFRIDEITT
DVDKTPYAYYFQQAGNGIFARQALLALVLNAELA
L"
gene 167279..167749 /gene="pyrI"
/locus-tag="y0162"
CDS 167279..167749 /gene="pyrI"
/locus-tag="y0162"
/function="enzyme; pyrimidine
ribonucleotide biosynthesis"
/note="residues 3 to 153 of 156
are 78.80 pct identical to
residues 1 to 151 of 153 from E.
coli K12 : B4244; residues 3 to
156 of 156 are 83.11 pct identical
to residues 1 to 154 of 154 from
GenPept : >gb|AAA26565.1| (J05033)
aspartate transcarbamoylase
[Serratia marcescens]"
/codon-start=1
/transl-table=11
/product="aspartate
carbamoyltransferase, regulatory
subunit"
/protein-id="AAM83756.1"
/db-xref="GI:21956831"
/translation="MMMTQDYKLQVEAIKCGTVI
DHIPAQIGFKLSSLFKLTATDQRI
TIGLNLPSSKRSGRKDLIKIENTFLTEQQANQLAM
YAPDATVNRIDNYEVVKNLTLSP
ERIDAVLTCPNNSNCISHNEPVFDSSFTVKAQRGEI

gene 167848..168273
CDS 167848..168273

SLKCKYCEKEFDHLTVLHAD"
/locus-tag="y0163"
/locus-tag="y0163"
/note="residues 11 to 141 of 141
are 83.20 pct identical to
residues 11 to 141 of 141 from E.
coli K12 : B4243; residues 14 to
141 of 141 are 85.93 pct identical
to residues 1 to 128 of 128 from
GenPept : >gb|AAL23277.1|
(AE008909) putative translation
initiation inhibitor [Salmonella
typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83757.1"
/db-xref="GI:21956832"
/translation="MISLSALRKSGVKMLRAIKT
KLAFAAIGPYVQGVQLGSMIMTSG
QIPIDPKTGLVADDIAAQARQSLENVKAIIVEAAG
LKVA DIVKTTVFKDLDNDFSIVNA
TYEAFTEHSAPFPARSCEVARLPKDVKIEIA
IAVRR"
/locus-tag="y0164"
/locus-tag="y0164"
/note="residues 62 to 143 of 158
are 31.70 pct identical to
residues 1565 to 1640 of 3016 from
GenPept : >dbj|BAAI17634.1|
(D90907) ORF-ID:srl1403 integrin
alpha- and beta- subunit domain
homolog [Synechocystis sp. PCC
6803]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83758.1"
/db-xref="GI:21956833"
/translation="MKLRTWLLIPIICSPFFWGS
TAIAKNGVAIPLPDKRVAVLSEGD
LESASVGTYSAIFKNDTFLDFIAGGVFSRDGSI
FQDNKGPRVEFTDINGDGNKELIV
SQLTAGSGNYLRLVDAFSLGPDSINKVLSIQSDTK
SDYISLLKELCIECILPIDAPPH"
/gene="treR"
/locus-tag="y0165"
/gene="treR"
/locus-tag="y0165"
/function="regulator; osmotic
adaptation"
/note="residues 1 to 316 of 317
are 62.02 pct identical to
residues 1 to 314 of 315 from E.
coli K12 : B4241; residues 1 to
316 of 317 are 62.02 pct identical
to residues 1 to 314 of 315 from
GenPept : >dbj|BAB38641.1|
(AP002568) repressor of treA,B,C
[Escherichia coli O157:H7]"
/codon-start=1
/transl-table=11

gene 168572..169048
CDS 168572..169048

gene 169282..170235
CDS 169282..170235

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/product="repressor of treA, B, C"
/protein-id="AAM83759.1"
/db-xref="GI:21956834"
/translation="MQNRLTIKDIARMGVGKST
VSRVLNNEGSVSPQTERVEAVIR
QHGTTPSKSARAMRGSDKVVGIIVSRLDSPSEN
QAVRTMLPLFYQQGYDPILMESQF
DTTLVSEHLHLQQRHVDGVILFGFSGLTAEMLA
PWQEKMVVLAREYRGFSVSCYDDE
GAIYLLMDKLRAQAGHRHISYIGVQSSDATTGMRR
YQAYLDYSQQHGHTPMVALGELSY
QSGFQALAPQVITPQTSALVCASDTIAMGVSKYLQ
QGEREQPIQVCGIGNTPLLHFLLF
PDTLTIELGYGRAGVKAQQLDQLSNSQLPIQQI
IIPGQLV"
/gene="treB"
/locus-tag="y0166"
/gene="treB"
/locus-tag="y0166"
/function="transport; transport of
small molecules; carbohydrates,
organic acids, alcohols"
/note="trehalose specific;
residues 13 to 483 of 483 are
80.46 pct identical to residues 2
to 472 of 473 from E. coli K12 : B4240; residues 13 to 483 of 483
are 80.89 pct identical to
residues 2 to 472 of 473 from
GenPept : >dbj|BAB38640.1|
(AP002568) trehalose specific PTS
system enzyme II [Escherichia coli
O157:H7]"
/codon-start=1
/transl-table=11
/product="PTS system enzyme IIBC"
/protein-id="AAM83760.1"
/db-xref="GI:21956835"
/translation="MRARNLYGKDDKMGKVQQD
IDQLLVLVGRENIAVTSHCITRL
RFVLKDPSIASPKEIENLMSMVKGCFNAQGFQVV
IGPEVDYKKALIAKIGQSEVDE
QTKLAARQNMTWFERGISHFHAEIFFPLLALISG
GLILGFRNVNGDIPMSEGKTLAQM
YPAWTIYDFWLGEAIFFFYLPAICWSTVKKM
GGTPVLGIVLGIITLVSQPLMNSYL
LGQQLPDVWNFGWFTIEKVGYQAQVIPSILAGLA
LGWIETNLKRKIIPAYLYLVVVPVV
SLLLAFLAHTLIGFFGRMIGDGVAWGVKAVMTG
SFAPVGAALFGFLYALPVITGVHQ
TTLAIDMQVMQSMGGTPVWPLIALSNIQAQSAVL
GIIIISSRKINEREISVPAASAYL
GVTEPAMYGINLKRYRFPMLCAMIGSALAGLICGL
TGVMANGIGVGGLPGILSIQPQFW
GIYAVAMLVAIVVPLALTILVYKRERRGELPV"
/gene="treC"
/locus-tag="y0167"
/gene="treC"
/locus-tag="y0167"
/function="enzyme; degradation of
small molecules; Carbon compounds"
/note="residues 7 to 553 of 555

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are 73.85 pct identical to residues 7 to 549 of 551 from *E. coli* K12 : B4239; residues 7 to 553 of 555 are 73.12 pct identical to residues 6 to 548 of 550 from GenPept : >emb|CAD06914.1| (AL627283) trehalose-6-phosphate hydrolase [*Salmonella enterica* subsp. *enterica* serovar Typhi] /codon-start=1 /transl-table=11 /product="trehalase 6-P hydrolase" /protein-id="AAM83761.1" /db-xref="GI:21956836" /translation="MNNPIPWQHGVIYQIYPKS FQDSTGNGYGDLAGVAQRQLDYLQK LGVDIAWLTPVYVSPQVNDGYDVADYCAIDPAYG TLDDFKRLVAGAHQRGIRIIIMDMV FNHTSTEHAWFKASQDRNSPYRQFYIWRDGDGGD GSLPNWNRSKFGHAWQWAHASQG YYLHLFLAPEQADLNNEHQFQVRDELKKVCEFWDL GVDGLRLDVINLVSKQQDFPNLDD GDGRRFYTDGPRIHEFLQELS RDVQFQPRLLMTVG EMSSTRLEHCQRYAALGGDELSTM FNFHHLKVDYLNGEKWSLMPNRVELKHIFNQWQ QGMHNRAANALFWCNHDQPRIVSR FGHEGALRLPAAKMLAMVLHGMQGTPYIYQGEEI GMTPNPNTDITQYRDVESLNMFAE LSVAGREPDELLAILAAKSRSRDNRTPMQWDSSDN AGFSQGTPIWIAPCSNYHEINVNAA LADADSVFYAQYLIALRKQYDIFTFGDYQDLC P QHPDLWCYLRSWQGKOLLVVANLS EEPQRWQPEGTLTLDGNWQLLMSYYDQS AFQPQDM ILRGYEGIYWVCCE" /gene="rnk" /locus-tag="y0168" /gene="rnk" /locus-tag="y0168" /function="regulator; central intermediary metabolism: Nucleotide interconversions" /note="residues 1 to 134 of 136 are 64.92 pct identical to residues 1 to 134 of 136 from *E. coli* K12 : B0610" /codon-start=1 /transl-table=11 /product="regulator of nucleoside diphosphate kinase" /protein-id="AAM83762.1" /db-xref="GI:21956837" /translation="MTKPTITINELDAERLDALL AQPAFAFGSVATALEELDRAEIL PPNEIPADVTMNSRVRFQFLDLNSQEEHIRTLYVP ASLKDSNEQLSVMAPLGAALLGLH VNDEISWKLPGGDETRITVLELLYQPE SAGEYHR"

| | | |
|------|-------------------------|--------------------|
| gene | 174176..174586 | |
| CDS | 174176..174586 | |
| gene | complement(174818..1752 | /gene="cybC" |
| | 10) | /locus-tag="y0169" |
| CDS | complement(174818..1752 | /gene="cybC" |
| | 10) | |

/locus-tag="y0169"
/function="enzyme; energy
metabolism, carbon: Electron
transport"
/note="residues 31 to 130 of 130
are 57.99 pct identical to
residues 1 to 100 of 100 from E.
coli K12 : B4236; residues 3 to
130 of 130 are 52.34 pct identical
to residues 1 to 128 of 128 from
GenPept : >gb|AAL23259.1|
(AE008908) cytochrome b(562)
[Salmonella typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="cytochrome b(562)"
/protein-id="AAM83763.1"
/db-xref="GI:21956838"
/translation="MSMGKTLMALITAALLSTSS
LVMAASVADDMETIAEHYGKVLA
DSTAIVKQDLQAMRVAAVDAQKGIPTKLKSKVED
SPEMKDFRHGMVDLIGEIDGALAL
ADQGKLDEAKQAAQDFKDTRNTYHKKYR"

gene complement (175412..1760 /locus-tag="y0170"
56)
CDS complement (175412..1760 /locus-tag="y0170"
56)
/note="residues 25 to 134 of 214
are 23.21 pct identical to
residues 51 to 159 of 320 from
GenPept : >gb|AAC06973.1|
(AE000710) pyridoxal phosphate
biosynthetic protein PdxA [Aquifex
aeolicus]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83764.1"
/db-xref="GI:21956839"
/translation="MIMPVLIRGSSNMIVMPSTY
SPATIAREFKVIHEFELSSMKYGV
IFDKNVPKAIIIRMNIESFNGIIPRHRIIAALDLV
AKQELGENVISVQRFWFQDSALFQV
EGMVVEQGARGKGLATLLYEELVVVKCGVILMSDN
KQYEAGKALWQRIAQESDKLAVFI
LDSDVGFQPYCGDRVPIYNKGKIPPEEKIWSLHPD
TTKVGWVVLVAENREKISQYC"

gene complement (176305..1776 /gene="pmbA"
45)
CDS complement (176305..1776 /gene="pmbA"
45)
/locus-tag="y0171"
/function="phenotype; proteins -
translation and modification"
/note="maturation of antibiotic
MccB17, see tld genes; residues 1
to 446 of 446 are 82.73 pct
identical to residues 5 to 450 of
450 from E. coli K12 : B4235"
/codon-start=1
/transl-table=11

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/product="PmbA/TldD family
protein"
/protein-id="AAM83765.1"
/db-xref="GI:21956841"
/translation="MKVVTQVAEQRKTLEQAVAQ
ALELARVGSDAAEVAVSKTTGIVS
STRFGEVENVEFNSDGALGITVYHQQRKGSASTT
DLNPDAVARTVQAALDIARYTSPD
PYAGPADKSLLAFDADPLDFHPGDLDAEQGILL
AARAEQAALQADKRITNTEGGSFN
SHYGIVFGVGNHGMQLQSYCSSLRHSLSSSVIAEHN
GDMERDYAYTIGRMEDLATPEWV
GEECARRTLSLSPRKLPMTQSPVLFAAEVATGL
FGHLVSAISGGNIYRKSTFLLDHL
GQQILPEWLTIEEHPHLLRGLASTPDFSEGVRTL
QREIVKDGVLTQYLTSYARKLG
LQSTGHAGGIHNWRIAGQGODFAGMLKQLDKGLV
VTELMGQQGVSTVTGDYSRGAAGFW
VENGEIQXPVSEITIAGNLKDMRLRNIVSVGSDIE
TRSNIQCGSVLFPVMKIAGE"
/locus-tag="y0172"
/locus-tag="y0172"
/function="phenotype; Not
classified"
/note="residues 3 to 183 of 184
are 78.02 pct identical to
residues 1 to 182 of 183 from E.
coli K12 : B4234"
/codon-start=1
/transl-table=11
/product="putative alpha helix
protein"
/protein-id="AAM83766.1"
/db-xref="GI:21956842"
/translation="MTMNQOPEDWLDDVPENKN
DDDEIINWVKSEIKRDAEALKDGL
TELVDLGNALERIPLDEDLAAIELAQKIKKEG
RRRQLQLIGKMLRARDVEPIQTL
DKLNKRHNQOISLFHKLETLRDRLLIAEGDEAIPT
VLELYPDADRQQLRSLSVRNAQKEQ
AANKEPKPSFRQIFSYSLRELAEKKQ"
gene complement(178486..1787 /locus-tag="y0173"
67)
complement(178486..1787 /locus-tag="y0173"
67)
/complement
/note="residues 6 to 87 of 93 are
53.01 pct identical to residues 6
to 88 of 90 from E. coli K12 :
B3239"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83767.1"
/db-xref="GI:21956843"
/translation="MVKVVFDFNHNIPDLPFYRA
FSQNFALEDFGANLDAWDVVVIG
EIALPVEIEFVHFSSRRHQRFFAAIVVLLLEEAEEE
LAGRLHFNVVDDEHIV"
gene complement(178772..1792 /locus-tag="y0174"
45)
complement(178772..1792 /locus-tag="y0174"
45)

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/function="enzyme; macromolecule degradation: Degradation of RNA"
/note="residues 1 to 156 of 157
are 47.43 pct identical to
residues 1 to 148 of 149 from
GenPept : >gb|AA86441.1| (M14442)
barnase (RNase) precursor
(*Bacillus amyloliquefaciens*)
/codon-start=1
/transl-table=11
/product="putative ribonuclease"
/protein-id="AAM83768.1"
/db-xref="GI:21956844"
/translation="MNKRMAILGAVLLIAGAW
QGIDGVTVRDIGSSAELERPALSA
SAATESLTOHQKVVKYLQTHHRLPDFYLTKKQAR
EQGWDAQKGNLCDVDLPKGKAIGGDR
FSNRERQLPDAKGRHWREADVNRCGRRGSDRLL
YSNDGLIYLTDHYKHFIEME"

gene complement(179440..1797 /locus-tag="y0175"
78)

CDS complement(179440..1797 /locus-tag="y0175"
78)
/note="residues 1 to 112 of 112
are 59.82 pct identical to
residues 374 to 485 of 486 from
GenPept : >gb|AAL44216.1|
(AE009270) succinate semialdehyde
dehydrogenase [*Agrobacterium*
tumefaciens str. C58 (U.
Washington)]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83769.1"
/db-xref="GI:21956845"
/translation="MIADANEQMVKVASEETFGPL
AACFRFSTEAEVIRQRANNTPFGLA
AYFYTQNLRQVRVSEALESGMIGVNECSVTEL
APFGVVKESGLREGSVLGLDEFM
EVKTLHLGNL"

gene complement(179775..1809 /gene="gabD"
08)

CDS complement(179775..1809 /gene="gabD"
08)
/locus-tag="y0176"
/function="enzyme; central
intermediary metabolism: Pool,
multipurpose conversions"
/note="NADP-dependent activity;
residues 23 to 366 of 377 are
56.06 pct identical to residues 15
to 360 of 482 from *E. coli* K12 :
B2661"
/codon-start=1
/transl-table=11
/product="succinate-semialdehyde
dehydrogenase"
/protein-id="AAM83770.1"
/db-xref="GI:21956846"
/translation="MPAQNPQHQQRQHDGIYHIG

YFVGKKWSQAQEQFDVYNPATGEL
 VARVAKSGKQETEAAIKAASEAFAWRKTPAKQR
 AEILQRWYLLIMEHQQSIAELMVS
 EQGKPLKEALVEVAYAASFQWFSEQAKRANGEI
 IPSAKEGARILATREPIGVVAIT
 PWNFPLAMLTRKLGPALAAGCTGLIKPANNTPLS
 AFALLALAEQAGVPAGVLNGVVGD
 THAISDAIMASSDVRKISFTGSTINVGKTLMRNAA
 ATMKRISMELGGNAPYIVFDDADL
 EAAVAGAMACKERFRNAQCVCVNRFYIQDAIYDE
 FVNRLAAEVKKLVGNMDKDVNMM
 GPLINLAGLEKVEEHVKDALEKGGRLLAGGIAMR
 WAVISSOR"

 gene complement(181175..1831 /locus-tag="y0177"
 30)

 CDS complement(181175..1831 /locus-tag="y0177"
 30)
 note="residues 9 to 650 of 651
 are 64.64 pct identical to
 residues 11 to 652 of 655 from E.
 coli K12 : B3240; residues 9 to
 650 of 651 are 64.79 pct identical
 to residues 11 to 652 of 655 from
 GenPept :
 >gb|AAG58368.1|AE005551-11
 (AE005551) orf, hypothetical
 protein [Escherichia coli O157:H7
 EDL933]"
 /codon-start=1
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 /protein-id="AAM83771.1"
 /db-xref="GI:21956847"
 /translation="MTHPSFIRLRFALKSFAIV
 AALFLGFHLQLETPRWSVLTAAIV
 SAGPFAAAGGEPEFGAIRHRGWLRRIIGTFIGCIG
 GLVIIIVLTIRAPVLTLMCCLWAG
 ICTWSSLVRVENSAYAFGLAGYTAIIIVTTGET
 PLLTQFAVERCESEIVLGIVCAVM
 ADLLFSPPRSIKQDIDRLVDKVLVDQYRLLQLCIQ
 PAEKSEIDRAWNELVKNTTSLNGM
 RSYLMMESSRWQRCNRRLQVLHTESTSLALITQACE
 TYLVMSNHPEVISAEALKMLSEPA
 QTPAEIHQQMKKLRQFIAASHSEAIPHTISSWVG
 AATRYLLSKGIQTNSNSINQVEED
 ILAGDAPVKPIASEGHAMINGLRTGIATAIGGL
 FWLWTGWTSGAGCMVMIAVVTSIA
 MRTPNRRMALDFLVGVIIALPIGALYFMFIIPS
 TQQSMLLLCISLGVLAIFIIGIEVO
 KRRRLGSILGTLASTINIIVLSNPIMIFNVRQFLDSA
 LGQIVGCFVSLIVLLLIRDNAKDR
 TGRTLLNRFVYSAVSALTNTKTRGENHNLPALYQ
 QLNQLMMMPADIDKYRLALTLLI
 AHQRRLNRTIEIPVNAELSAFHKQIRSTAERVITVN
 NDQKRRYYFARLLQELDQYQQKLV
 DYQAADAVIRPVKRLLTMRKYQSALI"

 gene complement(183132..1840 /locus-tag="y0178"
 67)

 CDS complement(183132..1840 /locus-tag="y0178"
 67)
 /function="putative membrane"
 /note="residues 1 to 311 of 311

are 72.66 pct identical to residues 1 to 310 of 310 from E. coli K12 : B3241; residues 1 to 311 of 311 are 100.00 pct identical to residues 1 to 311 of 311 from GenPept :
 >emb|CAC93154.1| (AJ414158)
 putative HlyD family secretion protein [Yersinia pestis]"
 /codon-start=1
 /transl-table=11
 /product="putative membrane protein"
 /protein-id="AAM83772.1"
 /db-xref="GI:21956849"
 /translation="MSTFSLKIIRVGITVLVVL
 AVIAIFNVAFTESPWTDRAKET
 ADVVAIAPDVSGLLTEVPVKDNOLVQKGQILFVI
 DQPRYQQALAEAADVAVYQTLAA
 EKQRESRRHRLGIQALSQEEIDQASNVLTQVQH
 QLAKAIAVRDLARLDLERTTVRAP
 AEGWVTNLNVHAGEFINRGATAVALVKKDTFYIL
 AYLEETKLLEGVRPGYRAEITPLGS
 NRIIHLGTVDSISAGVINSSSSADSKGLATIDNNL
 EWVRLAQRPVVKIHLDSEDQQLY
 PAGTTATVVITGPNDRDPHQASPMTKLMHRLREF
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 gene complement(184075..1842 /locus-tag="y0179"
 78)
 CDS complement(184075..1842 /locus-tag="y0179"
 78)
 /note="residues 1 to 66 of 67 are 81.81 pct identical to residues 24 to 89 of 90 from E. coli K12 : B3242"
 /codon-start=1
 /transl-table=11
 /product="hypothetical protein"
 /protein-id="AAM83773.1"
 /db-xref="GI:21956849"
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 LLISLALFFVVRRILQPTGIYEFV
 WHPALFNTALYCCLFYLTSLRFLS"
 /locus-tag="y0180"
 /locus-tag="y0180"
 /function="putative regulator"
 /note="residues 1 to 301 of 303 are 80.73 pct identical to residues 1 to 301 of 309 from E. coli K12 : B3243"
 /codon-start=1
 /transl-table=11
 /product="putative transcriptional regulator LYSR-type"
 /protein-id="AAM83774.1"
 /db-xref="GI:21956850"
 /translation="MERLKQMSVFAKVVVECGSFT
 AAARRLENSVSSISQTVSKLENEL
 NVKLLNRSTRRIGLTEAGRIYYQGCRRMLQEQQ
 VHEQLYAFNNTPTGTLRIGCSSTM
 AQNVLATMTADMVKAYPGLSVNLVAGIPAPDlia
 DGLDVIRGVGALQNSGLFSRRLGA

MPMVVCAAKSYLSQYGTAPAKPSDMANFSWLEYNV
 RPDSNFEELIAPEGITTTQISPQGRF
 VTNDSQTMIRWLKAGAGIAYTPLMWVIEEIKRGE
 VEILFKHYHSDFPRPVYALYTEKDK
 MPLKVQVICIDYLTEYFKRVADVYQDYR"
 /locus-tag="y0181"
 /locus-tag="y0181"
 /function="regulator"
 /note="residues 4 to 182 of 291
 are 26.76 pct identical to
 residues 8 to 200 of 303 from
 GenPept : >gb|AAC75958.1|
 (AE000375) putative
 transcriptional regulator
 LYSR-type [Escherichia coli K12]"
 /codon-start=1
 /transl-table=11
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 regulator"
 /protein-id="AAM83775.1"
 /db-xref="GI:21956851"
 /translation="MVHMHFISKNLLVFFTTVQEG
 SLTNAAVLFLTTTPPMRSRLKILE
 EELGFKLFLTRTTSGLKLITLEGAAFYQEIPTYVR
 LTEITKNYKKNKGNIINIAITYQLN
 SDHAGVICDYFIKKGNFNIELRENIGDISQMDIV
 ISTKEIKGYDFDTELTASCEIKLL
 YASHLNLDLPDRVEYLKLKLFIFIQSSIFCSSCCFKR
 FSHNLIQQGYSGNVLRIDDARVRH
 EIIKKGAGISLSTNYFFDKKKISHSTEISFISDI
 NFDITYYYIFKSSSVINKEFFIQYI
 TNNSLLQWQKAEKHH"
 gene complement(186780..1869 /locus-tag="y0182"
 41)
 CDS complement(186780..1869 /locus-tag="y0182"
 41)
 /codon-start=1
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 /db-xref="GI:21956853"
 /translation="MALFCFGLLMNRIISIRYNG
 CSMVDILHNLPFLYLGTLAWDVHQ
 QVLTMCLLK"
 /gene="tcaA1"
 /locus-tag="y0183"
 /gene="tcaA1"
 /locus-tag="y0183"
 /function="putative factor;
 extracellular functions; secreted
 proteins"
 /note="residues 182 to 557 of 774
 are 35.41 pct identical to
 residues 602 to 996 of 1095 from
 GenPept : >gb|AAL18449.1|
 (AF346497) toxin complex protein
 [Photobacterium luminescens]"
 /codon-start=1
 /transl-table=11
 /product="putative toxin subunit"
 /protein-id="AAM83777.1"
 /db-xref="GI:21956854"

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YEADPASIQSLFSPGRYLCELYHIV
AKELHDGNKLHIDKRRPDQLQELVLSNSNNQEV
SSLEILLNVLQTNAPLAKLAKDTE
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ALLAENNDPWANPITPALVOEQLG
LNPASYALIDIKSPLDNSAKRLAHATQLSVEQL
QWLKNNAIESSSDKDSPLRPEILT
IISEYRRLHQRYGLSVDPPIAIINAVNTTHTNEN
KTSFFQQIFSTLDVDAGFNFLDOG
SWEVIIRKALGITAEELLRIAKYCFGKSSISNVK
MNSKKFSQLYRMAMIPRTLGVGFS
QAEYLWOLYSHPDENIMEKIAQGNALTIIDAIIV
LENTLQWQMSEQKLDTITLQAMLTK
QYSTTATPELFNFNLSNIYQTLGKQVYESLKPML
YRSLANGFHLKANVVAGLVNWLA
NDSEFTLERFWONISMFTAEEPSLHQLEIHQPLL
IQCOKLSQYVLLIAQWAELSEQEIA
LILLPLNGIDNRGSAPSPTLKLSEFKLCCQE
AKVQSELFDIMQQLITDTNEKQE
KLRNSADKVIRSIAKSIGSINNSMDDIDSTISIR
NGSATLFPPEHPMYKALKLEVSNL
EKSQIQLEGKKEEEEIKLEQAKDNIQSLINNWDS
EIIIRLADAYHWIDINIANSIFILI
FGEKINFTHYENRNNDYHYEEHHYGYRFEQKPMYS
FDKKLTNGFGSILLLNKNHIYIAEK
LKIHPGTIIKIKNYIFDDKSNELENIANKLRVNL
"
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/locus-tag="y0184"
/function="putative factor;
extracellular functions; secreted
proteins"
/note="residues 1 to 1196 of 1197
are 42.03 pct identical to
residues 1 to 1187 of 1189 from
GenPept : >gb AAI18450.1
(AF346497) toxin complex protein
[Photurabdus luminescens]"
/codon-start=1
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LDTKIGHEVKTSPIAEAISSLQIYINRCVDGEEN
DLHEKNISTHESSDNFHLHGWNNSYN
KRYARWAGKEKLMYYAADYIDPTLRYNKTELFNT
FEQSINNSRLTEKSVKSALQSYLI
SYEKLAQIDTIKELYVENIKTHFFLGKTRESPCQ
YYWRSGEQLSNDSHHLRWSEWKV
NCNINGTEKFFFINLSWHRSSLYIDWINKFSIRT
DKDETTEKYHNRVYKNDONTWSE
LIINMDIGFKLSTSTEVITLPPFFVNQGDPAKE
EVENLFLTNGTISKRIESRLHGYI
NGHIKILCNDDGISPEIAEKLINGDNTIGEVKI
IENEKIISTINNEKGENKKINLID
KFEIRIFFYNELVASTIVFNRIKPEEKIIDELEDD
KISLLSPNSLPLKEKFQTSDELL |
| CDS | 189397..192990 | |

SYNTQKNNVKLNAFNGSYGIYLWELFFHIPLLAS
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 YRDGNGNLKEGDNLYWNILPLQQDFTAWDKNTL
 IQATDDDPVIAQMDDPMQYKLAIFM
 RTLDLIISQGDQAYQLERDTLAEAKIHYIQASQ
 LLGPRPNLNSSHQWENIKLAEESR
 QLENSHFPLPYNELLSSYWDKLEIRLYNLRHNLN
 LDGQFLHPLPFATPVDPKALQRQH
 GAGNGINSSEQIATAQTSLYRFPLLIERAKSAVS
 AVIQFGNSLQSVLERODNEAMTLL
 FQQQQQKVQLQHTKDIQNNDIQLQASLEATDSLX
 SAAEQRKRYKELLNDNGISSDEOL
 AINIRIASAALNGESLVPGLSLAVLDATPNVFGL
 ADGGSRWGAISQAVGWGMQSMAMA
 LETTAGVRDAKANYRSRAQEWTLQKDQADK DIEQ
 LAHQYTTSVQEQLNMAQKQLNLAEL
 EQGHADALYQMOSTRFTGKELYNWMAGRSLGLYF
 QLFDATQPLCLMAKAALKEVVDKA
 KTDGLFIRSGWNDLYQGLLAGEDLQLNQQLENV
 WLMEEQARLVERVTSLAOHYQQL
 SDHKFNLAIEIVTGYMAQDQDKTGNEQDFVELKN
 GTLITSLSIKGLNLVEDYDYPETMHL
 GDIRRIKQISVSLPALLGPYQDVOATLDYAGENT
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 /locus-tag="y0185"
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 /locus-tag="y0185"
 /function="putative factor;
 extracellular functions; secreted
 proteins"
 /note="residues 21 to 1511 of 1516
 are 48.90 pct identical to
 residues 1 to 1473 of 1476 from
 GenPept : >gb|AAL18487.1|
 (AF346500) toxin complex protein
 [Photorhabdus luminescens]"
 /codon-start=1
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 RTNAQVPRYDEYDEF LAPNGEVMVVAADPQGSIE
 RTEQSLNQEQQFSVIRYLPRIEGNF
 HRIEWWRPRTNNSQAFWLVHSSDGQKHCLGYS
 AARIADPLHPEHIAEWLLEESVSL
 SGHEIGYYQQAEDEQIIDEPSIYKAEKQNHPAAS
 AQRYLKRVVYGNRQAAELYCLTQ
 QPAPTSWLFSLIFDHGEYSNIAEQQPVIKKGKSW
 NFRQDAFSHFNNGFEVRTRRLCQO
 VLMYHNL SALKGDEPDAAOTLVSRLRLHYQHDAY
 ATQLVGCCQQLAHEPDGTKRSLPPL
 EFDYQDFSTRDALGWQPLTDWAEFNYQYQMVDLN
 GEGMPGMLYQDSGHWIYRPPVVRQP
 GTADGIFTGAAQRLPSPAMRENAMLDINGDGK
 LDWVISQPGLAGYFSRDPDLSRDP

| | |
|-------------|--|
| | <pre> DLSWTQF1PLSTLPAEYFHPQAQLVLAGSGLSD LALVGPKSVRVVTNLCDSFAAATQ VAQQDDITLPLPGVHTELVAFSDVMGSGQQHLV RIRHNNSVTCWPNLGHGRFGHPLSL PGFNQPVQEFPNPLAIYLADIDSGGTIDLITYATT QLLIYRNQSGNRFAEPLAIALPTG IRFDNSCQLSLADIQGLGVASIMLSVPFHPTTQHW RYDFVASKPYLLCTTNNNMGAESQ LLYRSRVQFWLDEKAQAAKQGRSLACQLPFFIHL LAQTTQFDEITGNSSLQTAARYFHG FYDGVQREFSGFGRVDLTDTSAQGSAERTAP TKSSRFWHTGRAGNETLWQSEYWO GDDQAYSSLPTRLTFKFINNTQGDELLSELDDNQT FWLHRALKGSSLRSELYGLDDSEL ATQPYSVNSSRQYVRQIQIQQSSADGQISPVALPMVL EQLSYHYERIAQDPQCSQQIVLRC NEYGHPLHSVTINYPRDKARISPYSWLAKEHWD SHFDEQQQQRLITESQQSYYHHEIS DKFYVLLGPLAGQRSDVLTYPDNFVPTAGIHWEEL QQPEGLLGKTAERTFTAAQQVFYT SDTIPGLVAYSQQAEDDGTDLVALDELLPANERK QQLIKAGYQIAPRLFARTGETDIW VAQSGFTDYGDASRFYRPIQSRTQLVGKTILEW DATCCAVSDIILADYSITHAEYDY RFITPYLLIDINDNOHYIELDALGRVTSSRFAGT EIDPQTNKVIETGFPSIAEQPFSA PNSVDKALSLENTRIPVAQFSVYQOPQSWMISQLQ DDIEIWIRANNITPEYLFCQNHLILI DNYYLCPPLALRRWGRQNQNLITEGVGLTLKNPMR QPPHLTVVVNDNYFSASAEPOQHQO TLAFSDGFGRVLLSARRVETGFSYSDPENGLLV DDKGNLVLQLEVQDRWAWSGRTEYD NKGLPFRRYQPYFFDNWIWLYIANN RTLKEFRRYADTHYDPLGREIKVITAKGYLRRTH YFPWFVISEDENDTASEITFPNP" </pre> |
| gene | 197671..197973 |
| CDS | 197671..197973 |
| | <pre> /locus-tag="y0186" /locus-tag="y0186" /function="phage-and prophage-related functions" /note="residues 14 to 94 of 100 are 45.67 pct identical to residues 12 to 92 of 101 from GenPept : >gb AAG55972.1 AE005330-4 (AE005330) putative holin protein of prophage CP-933X [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="hypothetical phage protein" /protein-id="AAM83780.1" /db-xref="GI:21956858" /translation="MHVQVIPIDFFFITWVIIIGTF SAWGGLVRYIVDQNNEYEEWSWVG VLCQVIVSAFTGLIGSLFTLETGSSRYITFAIAG LFGAMNTALKHLWQRFVSHSK" </pre> |
| gene | 197977..198387 |
| CDS | 197977..198387 |
| | <pre> /locus-tag="y0187" /locus-tag="y0187" /function="phage-and prophage-related functions" /note="residues 13 to 136 of 136 </pre> |

are 57.36 pct identical to residues 5 to 132 of 213 from GenPept : >gb|AAL41481.1| (AE009016) endolysin [Agrobacterium tumefaciens str. C58 (U. Washington)]"
 /codon-start=1
 /transl-table=11
 /product="hypothetical phage protein"
 /protein-id="AAM83781.1"
 /db-xref="GI:21956859"
 /translation="MDPMMNDKPTFRLSQISEHN
 LHHVHPDLVLIVRRALTLSHIDPR
 VIEGIRTPERQRQMVNLNGHSKTMNSRHLTGHAVD
 LAPMVNNRIPWDWWHAFTVHAKAM
 KQAAKAMELPLQWGGDWKNFRDGPHELPRECYP"

gene 198375..198743
 CDS 198375..198743

/locus-tag="y0188"
 /locus-tag="y0188"
 /note="residues 35 to 96 of 122 are 37.50 pct identical to residues 3 to 66 of 94 from GenPept :>gb|AAK81976.1|AF303741-42 (AF303741) 042R [Chilo iridescent virus]"
 /codon-start=1
 /transl-table=11
 /product="hypothetical"
 /protein-id="AAM83782.1"
 /db-xref="GI:21956860"
 /translation="MLPMISLSTLFGLGKSMML
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 RLEREKSSSELQKRRLRLAQKGNRCA
 EEPVPAAVIRMQQQSFSDGK"

gene 198730..198903
 CDS 198730..198903

/locus-tag="y0189"
 /locus-tag="y0189"
 /note="residues 8 to 32 of 57 are 43.99 pct identical to residues 632 to 656 of 732 from GenPept :>dbj|BAB15720.1| (AK024430) FLJ00019 protein [Homo sapiens]"
 /codon-start=1
 /transl-table=11
 /product="hypothetical"
 /protein-id="AAM83783.1"
 /db-xref="GI:21956861"
 /translation="MTVNECLPFPEVLLPPCQMP
 TFDVQTWGDYPHYVERTRLAMVRC
 NANRESALRFQQR"

gene 198944..201775
 CDS 198944..201775

/gene="tccC1"
 /locus-tag="y0190"
 /gene="tccC1"
 /locus-tag="y0190"
 /function="putative factor;
 extracellular functions; secreted proteins"
 /note="residues 13 to 699 of 943 are 53.30 pct identical to residues 12 to 694 of 760 from

| gene | 201800..204658 |
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| | GenPept : >gb AAL18492.1
(AF346500) unknown [Photorhabdus
luminescens]"
/codon-start=1
/transl-table=11
/product="putative toxin subunit"
/protein-id="AAM83784.1"
/db-xref="GI:21956862"
/translation="MPNILPTDLCANTPTLAIHD
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LRTDSVDGSSTLQLADSAAGRVTLT
LDAHHTRRWVEYETGEHSLGRPLSYHEQAKGGKL
TVTDRFVATNSEQDKSGNLNGOC
VRHYDSAGLQALINQSISGVPLQQQRRLTNPKG
PVDWFGEKENWGARLSEQQPFVSHS
TTDALGQLLTQDAKGHIQRMAYNRAQQLIGSWL
TIKNSAEQVILRSLTYSAAQOKLR
EESGNVNGVITEYRVEPOTQRLIGIKTRPAKKDRP
TRLQDRLRYDYPVGNIHLAIIHNAE
ATRFYRNQKIVPETTYRYDALYQOLIEATGREADT
NGIQNSQLPALASLNDNSNQFVNNT
RSYHYDRAGNLLKIQHTGASQYSTHITVSDSSNH
GIQQQEGLITARDIRSOFDAAGNQO
QLQPQQLPRLWNRSRNQLOQVEPVPRNDGISDSESY
LYDGGGSRVVKTSLHKTHNAIQTR
SVIYLAGLELRSQYNGNNLTEDFQVITVGAAGRA
QVRVLHWERGQPVDIVNDQLRYSF
DNHLSALIELSDGDIISQEEYYPFGGTAVLAS
RNTVEAKYKTVRYSKERDATGTLY
YYGYRYYQFWLGRWLSADPAFTIDGLNLYRVMVRN
NPVGLMDGGLMTDKLLAKHEANF
AKKNISMAELKSEIEKLGLLPADSKQLFLHNG
GESDDEPSGSSGSSGSSSEILENTS
PHKIKNHFHISEINLATMPRYYKDFSSTEMLE
SAERLKAYGSIDTLLTLDLTSEDI
PEFTSILADKGINYIAEKQYEIIDYFSEDELSS
NIDRIVNNMIKTIQNNNNHKVGIHCA
AGNGRSGLIATAMIINKKYTQSRINSFEENKLK
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/gene="tccC2"
/locus-tag="y0191"
/gene="tccC2"
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/function="putative factor;
extracellular functions; secreted
proteins"
/note="residues 13 to 723 of 952
are 52.56 pct identical to
residues 12 to 716 of 760 from
GenPept : >gb AAL18492.1
(AF346500) unknown [Photorhabdus
luminescens]"
/codon-start=1
/transl-table=11
/product="putative toxin subunit"
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/translation="MSTSLPTQLCANTPALTIDH
NRGLAIRTLAYNRDHNNETVDELI
SRNRYNASGQLIASRDPRLEVNDNFYQYSLSGV |
| CDS | 201800..204658 |

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 TTVDRFVATNSEQDKNCNLNGOC
 VRHYDSAGLQALISQSISGVPLQQQRRLTNPKG
 PVDWFGKEENWGARLSEQQPFVSHS
 TTDALGQLLTQTDACKHIQRMAYNRAQQLIGSWL
 TIKNSAEQVILRSLYSAAGQKLR
 EESGNGVITEYRYEPOTQRLIGIKTTRPAKKDRP
 TRLQDLRVDYDPVGNI LAIHNDAE
 ATRFYRNQKIVPETTYRYDALYOLIEATGREADT
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 RSYHYDRAGNLLKIQHTGASQYSTHTVSDSSNH
 GIQQQDGIIARDIRSOFDAAGNQO
 QLQPQPLRWNRSRNOLOQVEPVPRNDGISDSESY
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 SVIYLAGLELRQOHNDNNLITESFOVITVGAAGRA
 QVRVLHWEQGPVDIVNDLRLYSF
 DHNLGSALIELDSGDGIISQEYYPPFGGTAVLAS
 RNTVEAKYKTVRYSGKERDATGLY
 YYGYRYYQFWLGRWLSADPAGTI DGLNLYRVMVRN
 NPIWRDNNGGLTEEQINMYVNLF
 SNIGLKNDDELKSELLKYGLSEEQHQIYLNMLR
 FMQGQSSSSLFSPFSESSSSGQT
 QSVDSGYLSPVRYHFEDIKLATMHRYPKKQA
 SSDTITYSAEDLTEASPIKILIGL
 DLTSKNTOQYKSALAEKGKIKYITKEKYEITDFFE
 EGGLSTEQIDLTVNKILKLQKSDL
 VGIHCAGANGRSGVIASALSINKQYTTDKINSFD
 VTHSLRGSSILKDTQTYQVDTVTAK
 AVGIIREINPKAVERNQDVISLYRSHFLYTRKH
 TTSL"
 gene 204594..204800
 CDS 204594..204800
 /locus-tag="y0192"
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 /note="residues 1 to 65 of 68 are
 27.69 pct identical to residues
 146 to 210 of 237 from GenPept :
 >emb|CAB73875.1| (AL139078)
 putative integral membrane protein
 [Campylobacter jejuni]"
 /codon-start=1
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 /product="hypothetical"
 /protein-id="AAM83786.1"
 /db-xref="GI:21956864"
 /translation="MLFPYIDILIFYIQENTLHH
 YNLLILNTFPILNREGVYTRNTDF
 LKSLILTAALAKIGLNTIPMLCWH"
 gene complement(204861..2063
 /gene="tldD"
 06)
 /locus-tag="y0193"
 CDS complement(204861..2063
 /gene="tldD"
 06)
 /locus-tag="y0193"
 /function="phenotype; Not
 classified"
 /note="suppresses inhibitory
 activity of CsrA; residues 1 to
 481 of 481 are 84.40 pct identical
 to residues 1 to 481 of 481 from
 E. coli K12 : B3244; residues 1 to
 481 of 481 are 84.61 pct identical
 to residues 1 to 481 of 481 from

GenPept : >gb|AAL22237.1|
 (AE008855) suppresses inhibitory
 activity of CsrA [Salmonella
 typhimurium LT2]
 /codon-start=1
 /transl-table=11
 /product="PmbA/TldD family
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 /protein-id="AAM83787.1"
 /db-xref="GI:21956865"
 /translation="MSLSFVSEQLLTANKLNHQD
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 HEAVWLEDSIICKDGSYNIDQGVGVRAVSGEKTF
 AYADQITLNALQOSAHAARSIVRD
 TGNGKVHTLGEIAKYQALYPLLDPLQSLSRDKIA
 LLHHRVDKVARAADKRVQEVSASLT
 GYVEQILVAATDGTLAADVPRPLVRLSVSVLVEDN
 GKRERGACGGGRFGYDYFLETVD
 GEVRADNFANEAVRMLVNLSAIAAPAGAMPVVL
 GAGWFGVLLHEAVHGLEGDFNRR
 GSSVFSGGQMKGKLVASELCTVVDDDTMQGRRGSLA
 IDDEGVPGQYVNLIENGLIKGYMQ
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 LAGQSTPEDIIASVEYGLYAPNFG
 GGQVDTSGKFVFESTSEAYLIEKGKITHAVKGAT
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gene complement (206318..2071 /locus-tag="y0194"
 87)
 CDS complement (206318..2071 /locus-tag="y0194"
 87)

/function="enzyme"
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 GenPept : >gb|AAF93594.1|
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 protein [Vibrio cholerae]"
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 LLRARAIEQCVILAAAQVGRHGA
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 TLNKPLLNKPPSN"

gene complement (207184..2103 /locus-tag="y0195"
 75)
 CDS complement (207184..2103 /locus-tag="y0195"
 75)

/note="residues 37 to 1062 of 1063
 are 48.00 pct identical to
 residues 1 to 985 of 986 from E."

coli K12 : B3245; residues 1 to 1056 of 1063 are 49.00 pct identical to residues 244 to 1259 of 1266 from GenPept : >gb|AAL22238.1| (AE008855) paral putative protease [Salmonella typhimurium LT2]
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 /db-xref="GI:21956867"
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| | | |
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| gene | complement (211201..2126 | /gene="cafA" |
| | 70) | /locus-tag="y0196" |
| CDS | complement (211201..2126 | /gene="cafA" |
| | 70) | /locus-tag="y0196" |
| | | /function="structural component; cell division" |
| | | /note="residues 1 to 489 of 489 are 90.18 pct identical to residues 7 to 495 of 495 from E. coli K12 : B3247" |
| | | /codon-start=1 |

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protein"
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LMVQVVKDPLGTKGARLTTDITLPSRYLVLMGA
AHVGVSQRIESEAERERLKKTVA
YCDEQGGFIIRTAEEGIGEEELSADAALFKRLWT
KVQERKKRNITKYKLYGEMALAQR
VLRDFAGAAFLKIRVDSKLTYDLLVETREYIPE
MTDKLELYTGKQPIFDLYDVNEI
QRSLERKVELKSGGYLIIDQTEAMTTVDINTGAF
VGHHRNLEETIFNTNIEATQAIARQ
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SKDRVTKTSINGFSQLGLVEMTRKR
TRESIEHVLCHECPTCRGRGTVKSVETVCYEILR
EIVRVHAYDSDRFLVYASPAVGE
ALKGEESHALAEVEIFVGKQVKVQIEFLYQNQEKF
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gene complement(212660..2132 /locus-tag="y0197"
59)
CDS complement(212660..2132 /locus-tag="y0197"
59)
/note="residues 3 to 198 of 199
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residues 1 to 196 of 197 from E.
coli K12 : B3248"
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HQVMTAVALADRQNLMSAMVTDVTFRVLSPLEI
SDYIATGEPMDKAGAYGIGQKGCC
FVRAIAGSYHAVVGLPLVETHELLSHFIAQRNVR
GIHDH"
/locus-tag="y0198"
/locus-tag="y0198"
/note="residues 23 to 126 of 200
are 29.80 pct identical to
residues 226 to 324 of 454 from
GenPept :
>gb|AAF11838.1|AE002061-5
(AE002061) cell wall
glycyl-glycine endopeptidase,
putative [Deinococcus
radiodurans]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83792.1"
/db-xref="GI:21956871"
/translation="MSHLSQWPWPITCFADRPTPR
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 AILRNN"

gene complement (213267..2137 /gene="mreD"
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 /locus-tag="y0199"
 CDS complement (213267..2137 /gene="mreD"
 55)
 /locus-tag="y0199"
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 murein sacculus, peptidoglycan"
 /note="residues 1 to 162 of 162
 are 75.30 pct identical to
 residues 1 to 162 of 162 from E.
 coli K12 : B3249; residues 4 to
 162 of 162 are 77.35 pct identical
 to residues 5 to 163 of 163 from
 GenPept : >gb|AAL22241.1|
 (AE008855) rod shape-determining
 protein [Salmonella typhimurium
 LT2]"
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 protein"
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 note="residues 2 to 38 of 39 are
 44.73 pct identical to residues 73
 to 110 of 118 from GenPept :
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 unknown protein [Mesorhizobium
 loti]"
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 /db-xref="GI:21956873"
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 AGVDAAGAGGPIASAEGN"

gene complement (213752..2147 /gene="mreC"
 47)
 /locus-tag="y0201"
 CDS complement (213752..2147 /gene="mreC"
 47)
 /locus-tag="y0201"
 /function="structural component;
 murein sacculus, peptidoglycan"
 /note="residues 1 to 316 of 331
 are 81.32 pct identical to
 residues 1 to 316 of 367 from E."

coli K12 : B3250; residues 1 to 327 of 331 are 80.30 pct identical to residues 1 to 330 of 350 from GenPept : >emb|CADO7888.1| (AL627278) rod shape-determining protein [Salmonella enterica subsp. enterica serovar Typhi] /codon-start=1 /transl-table=11 /product="rod shape-determining protein" /protein-id="AAM83795.1" /db-xref="GI:21956874" /translation="MKPIFSRGPSLQLRLFFAAI
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 RLRELLGSPLRQDEQKMVTQVMSSGTDPYSDHVV
 IDKGSNSGVYEGQPVISDRGVVHQ
 VVAVKFTSRVLLICDASHALPIQVLRNDIRVIA
 AGSGCSDDLLLEHLPSNTDIRVGD
 VLVTSGLGGRFPEGYPVAVVSSVKVDNQRAYTVI
 QARPITADLQRRLYLLLWGA DRNG
 DMPMPDPEVRANERLAPMMSQVLPSADAMGPP
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| | | |
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94) | /locus-tag="y0202" |
| CDS | complement (214951..2159 /gene="mreB"
94) | /locus-tag="y0202"
/function="phenotype; cell division"
/note="septation function;
residues 1 to 347 of 347 are 99.13
pct identical to residues 21 to
367 of 367 from E. coli K12 :
B3251; residues 1 to 347 of 347
are 100.00 pct identical to
residues 1 to 347 of 347 from
GenPept : >emb CAC93135.1
(AJ414158) rod shape-determining
protein MreB [Yersinia pestis]"
/codon-start=1
/transl-table=11
/product="regulator of ftsI,
penicillin binding protein 3"
/protein-id="AAM83796.1"
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FMRPSPRVLVCVPVGATQVERRAIRESAQGAGAR
EVFLIEPMAAAIGAGLPVSEATG
SMVVDIGGGTTEVAVISLNGVVYSSSVRIGGDRF
DEAIINYYRRNNYGSILGEATAERI
KHSIGSAYPGDEVLEIEVVRGRNLAEGVPRGFTLN
SNEILEALQEPPLTGIVS AVMVALE
QCPPELA SDISERGMVLTGGALLRNLDRLMEE
TGIPVVVAEDPLTCVARGGGKALE
MIDMHGGDLFSEE" |

| | | |
|------|---|--|
| gene | complement (216331..2182 /locus-tag="y0203" | |
| | 47) | |
| CDS | complement (216331..2182 /locus-tag="y0203" | |
| | 47) | /note="residues 1 to 638 of 638
are 50.70 pct identical to
residues 1 to 641 of 646 from E.
coli K12 : B3252; residues 1 to
638 of 638 are 50.70 pct identical
to residues 1 to 641 of 646 from
GenPept :
>gb AAG58379.1 AE005553-1
(AE005553) orf, hypothetical
protein [Escherichia coli O157:H7
EDL933]"
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RYRQMVLPPLHOPGTEMHFNYIDPLGSYARIYA
AAILSLVVVVVIALTLLLSFRWLRD
QTVQEKLERRARRILNGEREHAVRSEDYEWPPC
ASRAIDHLLSELMEVRAERNRVDT
LIRTFAQAQDGATGLSNRQFFDNQLTTQLEETGAH
GVMVMVQLPDEFALENETHDQQQVQ
ELMSSSLVNLSTFVARYPSALLARYLNSDIAILL
PHKTLLKDADVMAAQLVNAVRTLPE
PHIIDRESLLHIGIVAYRSGESVEQIMDNAGQAT
KSAALYGGNGWVFDTQVERGRG
SVKWRITLEQTLASGGPRLYQKPVITVDGKISHR
EIIISRIYDGEQELLAAEFMPLVLQ
LGLGERYDRQKIDKIIPLLSSLWDETLAFSISVD
SLLHRPFQRWLRTLLQCKKSDRM
RIIFLAEADVCQHIEEIROMVRLLRGVGCKVMA
SQAGLTVVSTSYIKSLQVEMIKLH
PGVVRISINFRYENQLFVESLTGACAGTQTKVFAA
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/locus-tag="y0204"
/note="residues 1 to 324 of 325
are 74.38 pct identical to
residues 1 to 323 of 324 from E.
coli K12 : B3253; residues 1 to
324 of 325 are 74.69 pct identical
to residues 1 to 323 of 324 from
GenPept :
>gb AAG58380.1 AE005553-2
(AE005553) putative dehydrogenase
[Escherichia coli O157:H7 EDL933]"
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/translation="MRALILEQIEGRRTAEVRI
SASQLPAGNVTVDVNWSLNYKDA |
| gene | 218648..219625 | |
| CDS | 218648..219625 | |

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IGQSVLLTGWGVGENHWWGLAEQA
RVNGDWLVPMPDGLDARKAMIIGTAGFTMLCVM
ALEDGGVTPKSGEVVVTGASGGVG
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ILPRLSDYLDASRPLEKQLWAGAID
TVGDMSMLAKILAQMNYNGTVAACGLAGGYNLPTT
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are 75.44 pct identical to
residues 1 to 334 of 334 from E.
coli K12 : B1971; residues 62 to
394 of 394 are 79.04 pct identical
to residues 1 to 334 of 334 from
GenPept : >gb|AAL22246.1|
(AE008855) putative nitrate
reductase [Salmonella typhimurium
LT2]"
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NRFIGGGGLDYPVVEGLRLDEAMHP
LAFMVGVYVGKTLPPONGAPLRLMTPWKYGFKSI
KSIVHRLTRDOPPTTWNLSAPNE
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/note="residues 1 to 203 of 206
are 68.96 pct identical to
residues 1 to 203 of 211 from E.
coli K12 : B1972; residues 1 to
206 of 206 are 72.81 pct identical
to residues 1 to 199 of 199 from
GenPept : >emb|CAD07893.1|
(AL627278) putative membrane
protein [Salmonella enterica
subsp. enterica serovar Typhi]"
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/db-xref="GI:21956879"
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LPRYKKFRQWFR"
gene 221831..222283
CDS 221831..222283
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/function="enzyme"
/note="residues 1 to 146 of 150
are 73.28 pct identical to
residues 1 to 146 of 149 from
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(AF011408) type II
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salmonicida subsp. salmonicida]"
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/protein-id="AAM83801.1"
/db-xref="GI:21956881"
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FALQAAVNRLSLSKSN"
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/locus-tag="y0208"
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/function="carrier; biosynthesis
of cofactors, carriers: biotin
carboxyl carrier protein (BCCP)"
/note="carrier of biotin; residues
16 to 169 of 169 are 82.80 pct
identical to residues 1 to 156 of
156 from E. coli K12 : B3255;
residues 16 to 169 of 169 are
82.80 pct identical to residues 1
to 156 of 156 from GenPept :
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acetyl CoA carboxylase, BCCP
subunit, carrier of biotin
[Salmonella typhimurium LT2]"
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BCCP subunit"
/protein-id="AAM83802.1"
/db-xref="GI:21956882"
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VRISRAPAAPNYPMMQQPYAFAAAPQQQPALAAAV
APAPVAEEAAPAAISGHIVCSPMVG
TFYHTPSDAAKFVEVGQKVSVGDTLCLIVEAMKM
MNQIEADAKSGTVKAILVENGQPVE
FDEPLVIE"
gene 222396..222905
CDS 222396..222905
/gene="accB"
/locus-tag="y0208"
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/function="carrier; biosynthesis of
cofactors, carriers: biotin carboxyl carrier protein (BCCP)"
/note="carrier of biotin; residues 16 to 169 of 169 are 82.80 pct identical to residues 1 to 156 of 156 from E. coli K12 : B3255; residues 16 to 169 of 169 are 82.80 pct identical to residues 1 to 156 of 156 from GenPept : >gb|AAL22248.1| (AE008856)
acetyl CoA carboxylase, BCCP subunit, carrier of biotin [Salmonella typhimurium LT2]"
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/db-xref="GI:21956882"
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gene 222917..224266
CDS 222917..224266
/gene="accC"
/locus-tag="y0209"
/gene="accC"
/locus-tag="y0209"
/function="enzyme; fatty acid and
phosphatidic acid biosynthesis"

/note="residues 1 to 448 of 449
are 92.41 pct identical to
residues 1 to 448 of 449 from E.
coli K12 : B3256"
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biotin carboxylase subunit"
/protein-id="AAM83803.1"
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PLSDDTTKNKAFAKRIGYPVIKA
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QGNAYIYLAEADCMSQRHQKVEEAAPAPGITSEM
RRYIGERCACAKACMEIGYRGAGTPE
FLYENGEGFYFIEMNTRIQLVEHTVTTEMITGIDLK
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VECRNAEDPNITFLFSPGKJTRFHAPGGFGRVWE
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/note="residues 1 to 79 of 80 are
68.35 pct identical to residues 1
to 79 of 80 from E. coli K12 :
B3257; residues 1 to 79 of 80 are
69.62 pct identical to residues 1
to 79 of 80 from GenPept :
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(AE005553) orf, hypothetical
protein [Escherichia coli O157:H7
EDL933]"
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AN"
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small molecules; cations"
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are 82.83 pct identical to
residues 1 to 472 of 485 from E.
coli K12 : B3258"
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symporter"
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 FVGAMTVQFIGGARLLETAAGIPY
 DTGLLIFGISIALYTSFGFRASVLNDALQGLVM
 LIGTILLLVAVIAHAAAGLHLKAVET
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 IGLPHTAVRCISYRDSKAVERGII
 LGTIVVAILMFGMHLAGALGRAVLPDLKIPDQVI
 PTLMITVLPFAAGIFLAAPMAAI
 MSTINAQQLQSSATIVKDLYLNLPWAELKNERKL
 ARISSLSTLILGLLLLLAAWRPP
 MIIWLNLLAFCGLEAVFLWFLVGLGLYWERANAHG
 ALSAMIVGAVCYTVLASFDIKIAG
 LHPIVPSLTLNLLAFYIGNLFGDRARARHPAIVS
 AD"
 gene 227347..228267
 CDS 227347..228267
 /gene="prmA"
 /locus-tag="y0212"
 /gene="prmA"
 /locus-tag="y0212"
 /function="enzyme; ribosomal
 proteins - synthesis,
 modification"
 /note="residues 14 to 305 of 306
 are 85.27 pct identical to
 residues 1 to 292 of 293 from E.
 coli K12 : B3259"
 /codon-start=1
 /transl-table=11
 /product="methylase for 50S
 ribosomal subunit protein L11"
 /protein-id="AAM83806.1"
 /db-xref="GI:21956886"
 /translation="MVMAPIPALERIAMPWIQLK
 LNTTGNQAESLGDVLTVESGAVSVT
 FQDTHDNPVFEPLPGETRLWGDTDVIGLYDAETD
 MADVVAMLECHPQIGKGFIHKIEQ
 LEDKDWEREWMDNFHMPMFRGERLWICPSPRDVPD
 PTAVNVLMDPLGAFGTGTHPTTAL
 CLQWLDSDLNLNGKTLIDFGCGGSGILAIAAALKGA
 ARAIGIDIDPQAIQASRDNQRNG
 VSERLELYLARDQPAELSADVVVANILAGPLREL
 APLISVLPITTGGHLGLSGVLATOA
 AGVAQAYEDKFILDPVAEKEEWCRTIGKK"
 /locus-tag="y0213"
 /locus-tag="y0213"
 /note="residues 35 to 355 of 355
 are 87.85 pct identical to
 residues 1 to 321 of 321 from E.
 coli K12 : B3260; residues 35 to
 355 of 355 are 92.21 pct identical
 to residues 1 to 321 of 334 from
 GenPept : >gb|AAC77880.1|
 (AF040378) yhdG homolog [Serratia
 marcescens]"
 /codon-start=1
 /transl-table=11
 /product="putative dehydrogenase"
 /protein-id="AAM83807.1"

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/db-xref="GI:21956887"
/translation="MLFFQLVKVWPFIWAQKCV
YIAPLRTQCGHSLSMRIGHFQLTN
CLIAAPMAGITDRPFRALCHGMGAGMASEMLSS
NPEVWRDTDKSRLRMVHVDEPGIRN
VQIAGNDPDEMAAAAARINVASGAQIIDINMGCPA
KKVNRKLGSALLQHPDLVKQILS
AVVNAVDVFPVTLLKIRTGWSEHRCIEIAQLAEN
CGIQALTIHGRTRSCLFNGEAEYD
SIRAVKQTTSIPVIANGDITDPHKARAVLDYTGA
DALMIGRAAQQGRPWIFREIQHYLD
TGELLPPMPLGEVQRLLDGHIRELHDFYGPKGF
RIARKHVSWYLOEHAPNDQFRRTF
NAIEDASEQLEALEAYFENLA"
/gene="fis"
/locus-tag="y0214"
/gene="fis"
/locus-tag="y0214"
/function="factor; DNA -
replication, repair,
restriction/modification"
/note="DNA-binding protein; a
trans activator for transcription;
residues 1 to 98 of 98 are 97.95
pct identical to residues 1 to 98
of 98 from E. coli K12 : B3261"
/codon-start=1
/transl-table=11
/product="site-specific DNA
inversion stimulation factor"
/protein-id="AAM83808.1"
/db-xref="GI:21956888"
/translation="MFEQRVNSDVLTATVNSQD
QVTQKPLRDVSQALKNYFAQLNG
QDVSDLYELVLAEEVEQPPLLDMVMQYTRGNQTRA
LMMGINRGTLRKKLKYGMN"
/gene complement (230896..2313 /locus-tag="y0215"
72)
/CDS complement (230896..2313 /locus-tag="y0215"
72)
/note="residues 13 to 88 of 158
are 33.70 pct identical to
residues 4 to 89 of 134 from
GenPept : >dbj|BAB04617.1|
(AP001510) BH0898 unknown
conserved protein in B. subtilis
[Bacillus halodurans]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83809.1"
/db-xref="GI:21956889"
/translation="MNTENKKLSTLIGKIKHTIAK
SRLAAGYEDRNGINEHQVTPCHHA
LTLLGGDDFAESYLPFLRNNGFDLNGVRLFGYF
DDKGERDLRKQLADLKAFPELFP
DAFNNDWLIGETTDILIFNKNGSYENRDRIGL
DRLNESYDDIVGLLISLMPLE"
/gene complement (231438..2321 /locus-tag="y0216"
63)
/CDS complement (231438..2321 /locus-tag="y0216"
63)

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        /function="regulator"
        /note="residues 29 to 231 of 241
        are 36.71 pct identical to
        residues 9 to 215 of 223 from
        GenPept : >dbj|BABS3015.1|
        (AP003010) transcriptional
        regulator [Mesorhizobium lotii]"
        /codon-start=1
        /transl-table=11
        /product="putative transcriptional
        regulator"
        /protein-id="AAM83810.1"
        /db-xref="GI:21956890"
        /translation="MFCCITEAWYKKQPYCRTGIQ
LMLAGMGVIKPKETLRYQVENVLRQ
AIMSGRFTPGERLIERELCETLGVSRTSIREALR
RLEAEAKLVSIVPHKGPIVAIISRQ
EAAELFALRGILLEGFAAREPAQRATDVAIVHFAQ
AIQALRMRAGMTDKRAVKVLAKTDL
YDVLLDNCGNGLVKETLTSLSHRINLLRATSLMD
PQRLEPVSNIEIDDLYQALKARDP
AAERHVANAKEVALRIEETNAT"
gene    complement (232190..2335 /locus-tag="y0217"
54)
CDS      complement (232190..2335 /locus-tag="y0217"
54)
                    /function="transport; transport of
                    small molecules; carbohydrates,
                    organic acids, alcohols"
                    /note="residues 31 to 444 of 454
                    are 26.35 pct identical to
                    residues 35 to 452 of 461 from
                    GenPept : >dbj|BAB60327.1|
                    (AP000995) shikimate transporter
                    [Thermoplasma volcanium]"
                    /codon-start=1
                    /transl-table=11
                    /product="putative metabolite
                    transport protein, permease"
                    /protein-id="AAM83811.1"
                    /db-xref="GI:21956891"
                    /translation="METLSADSAITAAENDPLRD
VKRKNAIKGAFSEFIDMFDIYL
VIVLPPVLFYFQPPNLSSSTANILASLVFITTLL
GRPIGALLFGIMADRIGRRMASIY
SVSGFGVVTFIALIPGYETLGIAASYLLLVLRF
IDGIFLGGGTGAIPLALESVSKKE
QRGFVGGLLISGFPAAVYVAINLVAMLMFALIPLD
GLYSPTYAQWGRWIRPFVIGGLLAGF
LALYVFVNTESEVWQQGSSKKRAREKQPLSTLV
SGQSGRNLIWQVLLMMMSGFWLTQNL
ITLFPLTGLLINTLNMRGLQVTSILLVTYCVLFF
SYIGMGLGQKIGRRRFVMIAGPL
IATMGSALLYVLSHGDGLSFSTVMLLVCLLAVVV
TSPWGVIIITYINEHFATGV RATGF
GVGFSLSVIIPSYAFYMDWLSSVVVPELTAVVL
LALGGMIGTVGAIMGPETKEVDFT SSAG"
gene    complement (233708..2341 /locus-tag="y0218"
45)
CDS      complement (233708..2341 /locus-tag="y0218"
45)
                    /function="enzyme"

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/note="residues 21 to 141 of 145
are 48.36 pct identical to
residues 15 to 136 of 139 from
GenPept : >gb|AAK42990.1|
(AE006881) 4-carboxymuclactone
decarboxylase (pcaC) [Sulfolobus
solfataricus]"
/codon-start=1
/transl-table=11
/product="putative decarboxylase"
/protein-id="AAM83812.1"
/db-xref="GI:21956893"
/translation="MSNRVGYEIGRRVMMVAQDR
FERGFHNRKVVGLGAEHVETSWGN
DEFNRPVQKLITEYCWGEVWGDPA
LTFKTRSMLN
IGILTAMQHHELSLHVKGALRNG
VTREERAVLQLTQQYCGAPVALAAFRIASAAIK
AYDDEIADS"

gene complement (234281..2351 /locus-tag="y0219"
71)
CDS complement (234281..2351 /locus-tag="y0219"
71)
/function="enzyme"
/note="residues 6 to 290 of 296
are 34.58 pct identical to
residues 2 to 290 of 298 from
GenPept : >emb|CAD17800.1|
(AL646080) probable
3-hydroxyisobutyrate dehydrogenase
oxidoreductase protein [Ralstonia
solanacearum]"
/codon-start=1
/transl-table=11
/product="putative oxidoreductase"
/protein-id="AAM83813.1"
/db-xref="GI:21956894"
/translation="MKQLQRIGFIGLGMGTPMV
QLVKAGFELYLCDADITKVQILT
AELNAESLTVDNAASLDALITMLPNSEAVEQVLL
GSDGISGGWVAQLSQAAVVIDMSSS
DPERSRLAILLAVWELDYLDAPVSGGVVKAQNG
TLSILIGGEDRVLKSCYTALAAMG
EQILFVGPGAGSCHAAKALNNYVSATGLLATIEAL
HVAQRFGIEPEVMTEVLNTSTGRS
NTSNEKVRQFMLNGSYASGFTLQLMNKDLHIARN
LAQRNYPMRLGMHCVDVWDEVSR
RATPMADHTEMYRLLIDKEP"

gene complement (235236..2360 /locus-tag="y0220"
63)
CDS complement (235236..2360 /locus-tag="y0220"
63)
/note="residues 46 to 246 of 275
are 28.20 pct identical to
residues 34 to 254 of 262 from
GenPept : >gb|AAB89741.1|
(AE000998) *A. fulgidus* predicted
coding region AF1509
[Archaeoglobus fulgidus]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83814.1"

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/db-xref="GI:21956895"
/translation="MENRDMASASHENYRIFAICY
AHHHRLTRDNFLGGDPHDGPMPID
YFVVAIVGTTRTIMVDTGFDAAAMAHQRGRTITHC
IEDGLSQLGIDAGKIEDVIISHMH
YDHAGNHGLFPNARFHLDQDREMAFCTGRCMGHG
LSQAFDVEDVKAMVGRLFAGRLQF
HHGDAEIAPGISVHRVGHTDGLQIIRVHTARGW
VVLASDATHFYANIQQRYPILY
NVGVDLEGNTLYRWADSDFHIIPGHDPMLQRY
PAGTFETAAWIAQVDVAPLTQWT"
gene      236518..236991
/CDS       236518..236991

/gene="slyB"
/locus-tag="y0221"
/gene="slyB"
/locus-tag="y0221"
/function="putative membrane"
/note="residues 3 to 157 of 157
are 66.02 pct identical to
residues 1 to 155 of 155 from E.
coli K12 : B1641; residues 3 to
157 of 157 are 73.71 pct identical
to residues 1 to 155 of 155 from
GenPept : >emb|CAA42977.1|
(X60448) outer membrane
lipoprotein [Yersinia
enterocolitica]"
/codon-start=1
/transl-table=11
/product="putative outer membrane
receptor"
/protein-id="AAM83815.1"
/db-xref="GI:21956896"
/translation="MIMNKLAIAVALAATVLSGC
ANNTASGDTFTASQARQVQTVTYGA
SIVSARPVTIQGGNNNNVAGAIGGAVVGGFLGN
IGGGRGRNSLATAGGAVAGGVAGGG
IQSAMNRSEGVQLEIRRDDGSNIVVVQAQGPTRF
SAGQRVIIASDRSGTVTSPR"
gene      complement(237082..2372 /locus-tag="y0222"
79)
/CDS       complement(237082..2372 /locus-tag="y0222"
79)

/note="residues 41 to 57 of 65 are
76.47 pct identical to residues
1185 to 1201 of 1247 from GenPept
: >gb|AAL20679.1| (AE008778)
nitrate reductase 1, alpha subunit
[Salmonella typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83816.1"
/db-xref="GI:21956897"
/translation="MVFSSDFMGYVLHLMWINNL
LRQLNACGNLCNIFGGGRAYHHFV
THISPKPTHMIGGLRAISLRL"
gene      237428..237736
/CDS       237428..237736

/gene="cspI"
/locus-tag="y0223"
/gene="cspI"
/locus-tag="y0223"
/function="phenotype; Not
classified"

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/note="residues 33 to 102 of 102
are 82.85 pct identical to
residues 1 to 70 of 70 from E.
coli K12 : B1552; residues 33 to
102 of 102 are 98.57 pct identical
to residues 1 to 70 of 70 from
GenPept : >emb|CAB10779.1|
(Z97978) hypothetical protein
[Yersinia pestis]"
/codon-start=1
/transl-table=11
/product="cold shock-like protein"
/protein-id="AAM83818.1"
/db-xref="GI:21956899"
/translation="MSLLLSAQVRHPLKDRPRSL
HYCGKIIIEGNISMNSNKMTGLVKWF
DAGKGKFITPADGSKDVFVHFSAIQSNDFKTL
EGQNVEFSIENGAKGPFSAVNIAL "
gene 237921..238208
CDS 237921..238208
/gene="cspI"
/locus-tag="y0224"
/gene="cspI"
/locus-tag="y0224"
/function="phenotype; Not
classified"
/note="residues 26 to 95 of 95 are
84.28 pct identical to residues 1
to 70 of 70 from E. coli K12 :
B1552; residues 26 to 95 of 95 are
100.00 pct identical to residues 1
to 70 of 70 from GenPept :
>emb|CAB10779.1| (Z97978)
hypothetical protein [Yersinia
pestis]"
/codon-start=1
/transl-table=11
/product="cold shock-like protein"
/protein-id="AAM83818.1"
/db-xref="GI:21956899"
/translation="MPHKFYPSSLSSRLWRQLKII
EGSISMSNKMTGLVKWF DAGKGFG
FITPADGSKDVFVHFSAIQSNDFKTLDEGQNVEF
SIENGAKGPAAVNIAL"
repeat-region complement(238285..2389 /note="insertion element"
94)
/insertion-seq="IS1541a"
gene complement(238391..2389 /locus-tag="y0225"
00)
CDS complement(238391..2389 /locus-tag="y0225"
00)
/function="IS and transposon
related functions"
/note="IS1541a; residues 1 to 169
of 169 are 100.00 pct identical to
residues 1 to 169 of 169 from
GenPept : >gb|AAC82673.1|
(AF074611) transposase [Yersinia
pestis]"
/codon-start=1
/transl-table=11
/product="putative transposase"
/protein-id="AAM83819.1"
/db-xref="GI:21956900"

/translation="MRSGNCKCSTRNQKGVPMRD
 EKSLAHTRWNCKYHIVFAPKYRQQ
 VFYREKRRRAIGSILRKLCEWKNVNILEAEYCVDH
 IHMLLEIPPKMSVSGFMGYLKGKS
 SLMLYEQFGDLKFKYRNREFWCGRGYYVTVGKNT
 ARIQEYIKHQLEEDKMGQEQLSIPY
 PGSPFTGKR"
 /locus-tag="y0226"
 /locus-tag="y0226"
 /note="residues 61 to 115 of 120
 are 36.36 pct identical to
 residues 30 to 81 of 275 from
 GenPept : >gb|AAI48672.1|
 (AY071050) RE13795p [Drosophila
 melanogaster]"
 /codon-start=1
 /transl-table=11
 /product="hypothetical"
 /protein-id="AAM83820.1"
 /db-xref="GI:21956901"
 /translation="MGPFPDFLLNICSCTANC
 NKSKGVFITDPKLKALLNPQPSWG
 FSGHKKNLPPCRFCAYDITGD1KNTALPRAPES
 PADIIAAQKHNVTGQETV1WLNYL
 TILAGSSPFIHLEQCETVV"
 /locus-tag="y0227"
 /locus-tag="y0227"
 /note="residues 1 to 388 of 391
 are 58.50 pct identical to
 residues 1 to 388 of 391 from
 GenPept : >gb|AAI19518.1|
 (AE008722) putative ATPase
 involved in DNA repair [Salmonella
 typhimurium LT2]"
 /codon-start=1
 /transl-table=11
 /product="hypothetical"
 /protein-id="AAM83821.1"
 /db-xref="GI:21956902"
 /translation="MKKLIKRLIEIJKSGIELEDD
 DIIRHQLPYLKSETQDPVLVLFIVM
 AIEQGKFTQALDAIAITWLGSKQGVIQWQDIELAA
 CKLELKALEEQLSELIDKRNERIQ
 LLDDFNNDLVLVRGLPLMKQILNLRQLAESTLRK
 AEAEARRRERDYRNCQQYISQAID
 ELISLQKQRWLALPSISNDTIEIRNRIQQQTELIT
 ALLAEIKELENSFCTRNTTESTRKA
 REEAKEKEVYERQEQQTDAEQRQLNDNRKLSSSEQRQ
 DLKRLWRQASRLCHFDLVADAFKE
 KAHQLMVQLNQARQRGDFPFAIHALLESLKQGLEP
 LMASDLIDDLERLRRK1SDVRTQI
 DAILHEIDALKGEESWRLATSLPDKDWFKEQEN
 VLSKTLNILERQVEEASRVLYEA"
 gene complement (240536..2418 /locus-tag="y0228"
 82)
 CDS complement (240536..2418 /locus-tag="y0228"
 82)
 /note="residues 3 to 446 of 448
 are 52.78 pct identical to
 residues 1 to 449 of 452 from
 GenPept : >emb|CAC45768.1|
 (AL591786) hypothetical signal

| | | |
|------|--------------------------|--|
| | | peptide protein [Sinorhizobium
meliloti]" |
| | | /codon-start=1 |
| | | /transl-table=11 |
| | | /product="hypothetical" |
| | | /protein-id="AAM83822.1" |
| | | /db-xref="GI:21956903" |
| | | /translation="MHHMSKFLVLLASSIAFSTS
SWAQAVEVPAVLAGHAVLVPVKSTV
ATPSDAPTDLQOSGKYTSGQRVSALGSVAAKSAD
RLTGIGLPISGQPLQGHSGIKHMP
DGTYWVLTNDNGFGSKANSPDAMLYLNHYNIDFKN
GNVTPLQTFLHDPPDKVVFHIIN
ESTEKRYLTGSDFDPESFQFADDALWIGEFGPY
LIKADLNGKVLAVFETQVDGNVVK
SPDNPTLTLPGAPDGKQNFQVARSKGFEGMAVSP
DGSKLYPMLEGALWDGEKFENIDG
KRYLRVLEFDVKNQAWTGRSWQYVLEDNQNQNAIGD
FNLIDANHGLVIERDNGEFTADKA
CAAGAPTDKCFSQIAFKRKYKIAFSDDNVGKPV
EKVSYIDLNNIKDPQNLARKPLNN
GVLTFPFFTIENVDVVDA SHIIIVGNDNNFPSSS
RQPNEADDNEFILLDVVKALLSQ" |
| gene | 242133..242987 | /locus-tag="y0229" |
| CDS | 242133..242987 | /locus-tag="y0229"
>note="residues 2 to 280 of 284
are 70.25 pct identical to
residues 17 to 295 of 304 from E.
coli K12 : B2989; residues 2 to
280 of 284 are 72.04 pct identical
to residues 1 to 279 of 288 from
GenPept : >gb AAL22014.1
(AE008844) putative glutathione
S-transferase [Salmonella
typhimurium LT2]" |
| | | /codon-start=1 |
| | | /transl-table=11 |
| | | /product="hypothetical protein" |
| | | /protein-id="AAM83823.1" |
| | | /db-xref="GI:21956904" |
| | | /translation="MMKDNEYQPPKIWENNAG
GVWSKINRPTAGARYEADLPVGKH
PLQLYSMGTPTNGQKVITILLELLALGEKGAEYDA
HLIRISEGEQFSSGFVSNPNSKI
PALMDYSSSTPPVRVRFESGAILLYLADKFHGFLPK
SHAARTEALNWLFWLOGAAPYLG
GFGHFYHYAPVKIEYAIADRTMEAKRQLDLLNTQ
LKTTHEYIAGDEYTIAIAIWPWYG
SLVLGQYEAGEFELDVKSYPHLIRWTETIAKRPA
VQRGRIVNRTWGAPEEQLPERHDA ADFDRLIK" |
| gene | complement (243177..2437 | /locus-tag="y0230" |
| CDS | 82) | |
| | complement (243177..2437 | /locus-tag="y0230" |
| | 82) | |
| | | /note="residues 14 to 194 of 201
are 44.75 pct identical to
residues 14 to 194 of 200 from
GenPept : >emb CAC95734.1
(AL596165) similar to putative
sugar-phosphate isomerase
[Listeria innocua]" |
| | | /codon-start=1 |

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/db-xref="GI:21956906"
/translation="MSQNKEWLAASDAWMIYSRE
LAALKENVDQQVWLQVLDAEAECR
GKIAVTGVTSGIAARKVAHMLACVEQPAIYLNA
TDAAHGDLGFLGAQDIIILISRGG
NSDELTLLPTLQRKQVKIISVTENEQSIAAQVS
ALVLKTHVKQEIDPLNMLATTSLIV
LVLALFDAICACLMARTGFSKETLLAVHPGGDVG
MVLRKQQ"
gene complement (243779..2454 /locus-tag="y0231"
31)
CDS complement (243779..2454 /locus-tag="y0231"
31)
    /function="enzyme"
    /note="residues 8 to 548 of 550
are 50.44 pct identical to
residues 13 to 566 of 569 from
GenPept : >emb|CAB81024.1|
(AL161576) putative protein
[Arabidopsis thaliana]"
/codon-start=1
/transl-table=11
/product="putative sugar kinase"
/protein-id="AAM83825.1"
/db-xref="GI:21956907"
/translation="MRDKTMASYFIGVDVGTGSA
RAGVFDLQGRMVQGASREITMFKP
KADFVEQSSENIWQAVCNAVRDAVNQADINPIQV
KGLGFDATCSLVVLDKEGNPLTVS
PSGRNEQNVIVWMMDHRAITQAERINATKHPLEF
VGGVISPEMQTPKFLWLKQHMPT
WSNVGHLFDLPDFLTWRATKDETDSLCTVCKWT
YLGHEDRWDPSYFKLVGLADLLDN
NAAKIGATVKPMGAPLGHGLSQRRAASEMGLIPGT
AVSVSIIDAHTIGILGAGSVIG
ENANFDERRIALTGGTSTAHHMMSRSAHFISGIWG
PYYSAILPEYWLNNEGGQSATGALI
DHIIQSHPCYPALLEQAKNKGETIYEALNYILRQ
MAGEPEENIAFLTDNDIIMLFYFHGN
RSPRANPNLTGIIITGLKLSTTPEDMALRYLATIQ
ALALGTRHIIETMNQNQNYNDTMM
ASGGGTKNPIFVOEHANATGCAMLLPEESEAMLL
GSAMMGTVAAAGVFESLPEAMAAMS
RIGKTVPQTNKIKAYYDRKYRVRFHQMYHDHMRY
QALMQEGA"
gene complement (245435..2463 /locus-tag="y0232"
88)
CDS complement (245435..2463 /locus-tag="y0232"
88)
    /function="transport; transport of
small molecules; carbohydrates,
organic acids, alcohols"
    /note="residues 20 to 310 of 317
are 58.76 pct identical to
residues 16 to 306 of 318 from
GenPept :
>gb|AAG54673.1|AE005211-8
(AE005211) putative permease
component of transport system,

```

probably ribose specific
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="putative permease of ABC
transporter"
/protein-id="AAM83826.1"
/db-xref="GI:21956908"
/translation="MTWLNRТИPDDRIIRLQLLI
LIAVMLVSLTLGQRFFSLGNFQS
MSSQLPILGMLALGMGLTMLTGGINLSIAGANA
CSLVMAAIIVSHPGOPAFLLLA
AGLLVAI GTLNGVLISVIGVSPILATLGTM
ITGLNILL SNGDVISGFPPIQYI
GSGDIVGIPVAMILFLVAA GLWVLLHEHTLGRS
IYLVGSNEQATRFSGVNTHRVQIA
VYILSALLGWGAII LMMAKFNSAKAGYGE SYLLV
TILASVLGGINPDGGFGRIIGLIL
ALVVLQLLESGLNLLGVSSYLTMA LWGGVLILFI
ALQNRKA"

gene complement (246390..2473 /locus-tag="y0233"
79)
CDS complement (246390..2473 /locus-tag="y0233"
79)
/function="transport; transport of
small molecules; carbohydrates,
organic acids, alcohols"
/note="residues 6 to 321 of 329
are 57.59 pct identical to
residues 1 to 316 of 323 from
GenPept :
>gb|AAG54672.1|AE005211-7
(AE005211) putative permease
component of transport system,
probably ribose specific
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="putative permease of ABC
transporter"
/protein-id="AAM83827.1"
/db-xref="GI:21956909"
/translation="MDKLKLRLQLTGHHFYLGLL
VLLAIGL SVQSPEFLT LGNLTDV
ATSYA IGL ILACGLF VVLTAGG IDISFP AVTAIA
QYVM ASW VIT QGG SFPL ALVMAMA
VGLLL GLING LLYV NWKVP AII ITI ATLN LFYGL
L VYFT NGTW LYGF PDWM TGINWF
SFEGSDG DYD GLT LPL CLAG IIIFT GVM MN YTR
LGRQIF AMGS NKA DAS RLG INIFR
LHLV YVGY MG ILAGV AAVVQA QIS QSVAP NSLMG
FELTV LA VV VL GGTS MGG RR GS LT
GTVL GVMLLA FQNL GTL LS VSSY WHTV FSG VII
LVS ISTA WNE KR KLL REH"

gene complement (247372..2488 /locus-tag="y0234"
68)
CDS complement (247372..2488 /locus-tag="y0234"
68)
/function="transport; transport of
small molecules; carbohydrates,
organic acids, alcohols"
/note="residues 116 to 498 of 498

are 61.19 pct identical to residues 9 to 392 of 392 from GenPept :

>gb|AAG54671.1|AE005211-6
(AE005211) putative ATP-binding component of transport system, probably ribose specific [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="putative ATP-binding protein of ABC transporter" /protein-id="AAM83828.1" /db-xref="GI:21956910" /translation="MTQATAFITLENISKRFPGV LALDGVLNLTLNKGEVHCLAGQNGC GKSTIIVISGVYQPEKGASILIDGKLLHQLTPQ LSFYYGVQVIYQDLSLFPNLTVAE NIAVHRYLPGGDFWVKRKSMRERALAAMQRVGVT LLDLKVQEQLSIADQLVACIRAI AADARLVIMDEPTASLTSGEVKGGLNVVRDLKSQ GICVVVFVSHRLDEVMEVADRISVM RDGKWWGTVQASELDSHELAFLMTGQRFTYRPLP PLAAKAFLLETRKLSRGEOFNRNI DLT LHQGEIVSITGLLGAGRTELCLSLSFGMTQPE SGEIFVAGEPVFRHNRAIRNGI GYVSEDRLTQGLIMEQSIVDNTIVSVFDQLHTRS GLLDHSKAALAVNKLVQDNLNIKVS DTALPVKTLSSGNGNAQRIAIAKWWATQPRILILDS PTVGVDIANKEGIYHIAKALAEQG MAVLMICDEIPEAYYNSHRLVLMRKGELIAEFYP HQCTEQQIAEVVNG"

gene complement (249072..2501 /locus-tag="y0235"
30)

CDS complement (249072..2501 /locus-tag="y0235"
30)

/function="transport; transport of small molecules; carbohydrates, organic acids, alcohols"
/note="residues 25 to 350 of 352 are 53.37 pct identical to residues 5 to 327 of 328 from GenPept :
>gb|AAG54669.1|AE005211-4
(AE005211) putative periplasmic binding protein, probable substrate ribose [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="putative periplasmic binding protein of ABC transporter" /protein-id="AAM83829.1" /db-xref="GI:21956911" /translation="MQNHNKISYLATVPLPERKQE GIAMKFNLALLNCIVSACMLFTT QTLAAEKKHEIAVVAKVTGIPWFTRMEGVVNNEAA KKLNVNAYQVGPATPDPQAQQVKVI EDLIAKNDAAIIVVPNDAKVLEPVVLKKAQEKGIV VLTHESPQRIQGQWDVETIDSEKY AQANMDELAKAMGNKGGYAIYVGSLTVPLHNAWA

DYAIKYQKEKYPEMFEVTPLPVA
 ENIDKSYSTLDMKTYPMQKGIIGFGSLGPIGA
 GQAVAKKRKRDQIAVVGIAAMPAQA
 APYLMRGDIKKALLWDPKDAGFAVVEIANQLNG
 QKVTEDLTIDGLGKADVDSKNGVI
 RFNKILEVTKONAKTTLGF"
 /gene="ddg"
 /locus-tag="y0236"
 /gene="ddg"
 /locus-tag="y0236"
 /function="putative factor"
 /note="residues 25 to 333 of 333
 are 66.66 pct identical to
 residues 20 to 327 of 328 from *E.*
coli K12 : B2378; residues 28 to
 333 of 333 are 66.66 pct identical
 to residues 1 to 305 of 306 from
 GenPept : >emb|CAD07638.1|
 (AL627274) putative
 acyltransferase [*Salmonella*
enterica subsp. *enterica* serovar
Typhi]"
 /codon-start=1
 /transl-table=11
 /product="putative heat shock
 protein"
 /protein-id="AAM83830.1"
 /db-xref="GI:21956912"
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 LTWFLGLVLFLLVQLFYPLLNKLGVWLGRRTSMRF
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 EQTIIGNFESLGMGLLETGMAFWFSDTRIQRWF
 VSGLENLKRQQGKGRCGVLYIGVHF
 MSLELGGRVMGQCQPMMAMYRPHNNKVMELVQTW
 GRMRSNKAMLDRLRDLRGMVRAALKQ
 GEAVWFAPDQDYGPRGSVFAPLFAVEHAATTSGT
 FMLARLAKPALLPLVLLRKKEGRG
 YDLLIQPALEYDPIIDDEIAASYMNKVIEKEIMR
 APEQYLWLRRFKTRPIGEPSLY"
 /locus-tag="y0237"
 /locus-tag="y0237"
 /note="residues 186 to 247 of 431
 are 26.15 pct identical to
 residues 515 to 579 of 865 from
 GenPept : >dbj|BAB73440.1|
 (AP003587) ORF-ID:all11741 probable
 proteinase [*Nostoc* sp. PCC 7120]"
 /codon-start=1
 /transl-table=11
 /product="hypothetical"
 /protein-id="AAM83831.1"
 /db-xref="GI:21956913"
 /translation="MKGKRAVGVVGITAHFILWF
 NRSNVALIPFFEGPSIMKSLILL
 ALLIPASVTANTLSPVKDTPKPALIDSLSATFAI
 DKIAMLKEKGANESENLYLPFEOT
 KDGLAILFDINQDGKIDALVPFTWEGLNGLDQE
 IPSNDWYSYYAIYLQDDQGWKQVG
 QIPTGTTFTTDNQTLTNIEDGVIVYGEIMPRMTDD
 DPQPQWVLRARPEKDNLLLVPPIPT
 PQPLANALTNLNSKKRPLTRNALVTAFGEPINIG

DNYFLVDGDCVGHPDWKYYQYPGA
AFNVSQNDNSVGVSFHIQIPDNLSLVLGDLTITQ
KTSAHQLIKALSQNDSFTSRTST
DLRTDLGQSSPYFDDANDIFALRLPYIAGFEAW
AKKNEAREVPNDEEADTFTRQFYF
TTTIGVAPIQNSPTRLMFYFLGDKMVALSVIYDD
GQVCI"

gene complement (253332..2550 /locus-tag="y0238"
02)
CDS complement (253332..2550 /locus-tag="y0238"
02)
/note="residues 8 to 554 of 556
are 75.13 pct identical to
residues 1 to 547 of 549 from E.
coli K12 : B4065; residues 5 to
555 of 556 are 74.95 pct identical
to residues 13 to 563 of 563 from
GenPept : >emb|CAD09253.1|
(AL627282) putative
sodium/hydrogen exchanger family
protein [Salmonella enterica
subsp. enterica serovar Typhi]"
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/db-xref="GI:21956915"
/translation="MWSLKEESMEIFFTILILIV
VSLSGVTVRMLLPFOVPLPLMQIVC
GALLAWPNFGLHVNFDPPELFVLVFLPPLFADGW
KTPTREFIHHGREILGLALALAVLV
TIVGIGYLIIYWMPGPILVAFAFALAALVLSPTDAV
ALSGIVGRGRIPKSIMGVLEGEAL
MNDASGLVALKFAIAVAMGTMIFTVSGATLEFLK
VAIGGLLAGVAITWLYSKSLRIMS
RWSGDDPATQIVLLLLLPFASYLVAEHLGVSGIL
AAVAAGMTISQSGIIRNAPLAMRL
RADSWWSMLEVFVNMGMVFILLGLQLPGILETSIT
QAELDPTIQTWNLFADVAIIYGA
LLLRFGWLMWSMKKISKRVLTKRPQLQFSDYTTREL
WVASFAFGVRGAITLAGVLSIPLFL
SDGSAPFSRYOLVVIATGVILLSVIIGVIALPPL
LRGVVVADKSASREEIRLARAAMA
EVAIVSLNKMEERLMTSSEENIDSELLKEVSSRV
IGTLRRRTGSKDEVNTLIENLE
RRFRLTALRAERGELYHLRATQKISNETLQKLLH
DDLILLEALLIEKG"

gene complement (255330..2566 /locus-tag="y0239"
85)
CDS complement (255330..2566 /locus-tag="y0239"
85)
/note="residues 4 to 451 of 451
are 85.04 pct identical to
residues 2 to 449 of 449 from E.
coli K12 : B4064; residues 9 to
451 of 451 are 87.35 pct identical
to residues 13 to 455 of 455 from
GenPept :
>gb|AAG58013.1|AE005518-7
(AE005518) Z4223 gene product
[Escherichia coli O157:H7 EDL933]"
/codon-start=1

| | | |
|--|--|---|
| | | /transl-table=11
/product="putative transporter"
/protein-id="AAM83833.1"
/db-xref="GI:21956916"
/translation="MSSSNPQAQPKGTLDAFFKL
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VIVVPSMLGKAGFPPTAVFVATCLVAGLGSLLMG
LWNLPMAIGCAISLTAFTAFSLV
LGQQISIPVALGAEFLMGVLFTIISVTGIRSWIL
RNLPMPGVAHGTGIGIGLFLLLIAA
NGVGLVIKNPIEGLPVALGAFTSFVIMTLLGLA
VIFGLEKLRVPGGILLVVVAISVI
GLIFDPSVTYQQLFAMPSSLADANGDSLIFSLDIM
GALQPVVLPSVLALVMTAVFDATG
TIRAVAGQANLDDKGQIISGGKKALTTDSVSSIF
AGLVGAAPAAVYIESAAGTAAGKK
TGLTATTVGILFLFLSPLSYLVPAYATAPAL
MYVGGLMLSNSVSKLDFEDFVDAMS
GLLCAVFIIVLTCNIVTIGMLGFSSLVIGRVCSCGE
WRKLNNGTVIIAVALVAFYAGGW I"
/locus-tag="y0240"
/locus-tag="y0240"
/note="residues 7 to 66 of 67 are
38.33 pct identical to residues 26
to 85 of 86 from GenPept :
>gb AAG54551.1 AE005201-4
(AE005201) damage-inducible
protein J [Escherichia coli
O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="putative DNA-damage
inducible protein"
/protein-id="AAM83834.1"
/db-xref="GI:21956917"
/translation="MANAKALGLDLSTVIRMVVN
RLAVNAELPIDLLQPNQETLQAIR
DLENGVEVYRVDSVDAKRDLGW"
/locus-tag="y0241"
/locus-tag="y0241"
/note="residues 2 to 27 of 27 are
57.69 pct identical to residues 73
to 98 of 98 from GenPept :
>gb AAF96231.1 (AE004370)
conserved hypothetical protein
[Vibrio cholerae]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83835.1"
/db-xref="GI:21956918"
/translation="MPDLLLIYQRTDSEIKLYRV
GSHSDF"
gene complement (257961..2588 /gene="ssuB"
15)
/locus-tag="y0242"
CDS complement (257961..2588 /gene="ssuB"
15)
/locus-tag="y0242"
/function="transport of small
molecules; carbohydrates, organic
acids, alcohols" |
|--|--|---|

/note="residues 22 to 256 of 284
are 72.34 pct identical to
residues 8 to 242 of 255 from E.
coli K12 : B0933; residues 16 to
260 of 284 are 72.24 pct identical
to residues 11 to 255 of 274 from
GenPept :
>gb|AAOG06830.1|AE004765-3
(AE004765) probable ATP-binding
component of ABC transporter
(*Pseudomonas aeruginosa*)"
/codon-start=1
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/product="putative ATP-binding
component of a transport system of
aliphatic sulfonates ABC
transporter"
/protein-id="AAM83836.1"
/db-xref="GI:21956919"
/translation="MASGLSTKIRRSMAMTTLTHI
PQGTPILESIGKRYGNRTVLNDNL
QLRITAGQFVAVVGRSGCGKSTLLRLLAGLEAAS
DGTLLSGNALLSHAKDETRLMFOE
ARLLWPKVVIDNVGLGLRGHWRDEALQVLDTVGL
ADRANEWPAAALSGGOKQRVALARA
LIHRPRLLLDEPLGALDALTRIEMQGLIERLWQ
QHGFITVLLVTHDVSEALIADRVL
LIEEGRIGLDLAIDLPRPRRKGSAKLAALAEAEVL
ERVLPSPQGIEASRQGIKASRQGT ATSSRRVAN"

gene complement (258773..2595 /gene="ssuC"
70)
CDS complement (258773..2595 /gene="ssuC"
70)
/locus-tag="y0243"
/function="transport of small
molecules; carbohydrates, organic
acids, alcohols"
/note="residues 1 to 260 of 265
are 79.61 pct identical to
residues 15 to 274 of 278 from E.
coli K12 : B0934; residues 2 to
264 of 265 are 80.98 pct identical
to residues 1 to 262 of 262 from
GenPept :
>gb|AAOG06831.1|AE004765-4
(AE004765) probable permease of
ABC transporter (*Pseudomonas
aeruginosa*)"
/codon-start=1
/transl-table=11
/product="putative transport
system permease protein of
aliphatic sulfonates ABC
transporter"
/protein-id="AAM83837.1"
/db-xref="GI:21956920"
/translation="MMTISAQRILHRLAPWILPV
ALVVGVQVAVEAGWLNSRILPAPS
AVVTAFWALKSGELWQHLTISSWRALIGFSIGG
SIGLVLGVITGLSRNGERLLNNSSV
QMIRNPVPHLALIPLVWFGIDESAKIFLVALGT

LFPIYLNTYHG1KNIDSGLLEMAR
SYGLSGFRLLTQVVLPGALPSIMVGVRFLGFMW
LTLIVAAATNSGIGYLAANNARE
FLQTDVVVAIVLYALLGKLADGSAQLLERVWLR
WHPAYQQKSGEAQ"

gene complement (259579..2607 /locus-tag="y0244"
27)
CDS complement (259579..2607 /locus-tag="y0244"
27)
/note="residues 1 to 382 of 382
are 78.79 pct identical to
residues 1 to 381 of 381 from E.
coli K12 : B0935; residues 1 to
382 of 382 are 81.93 pct identical
to residues 1 to 382 of 382 from
GenPept :
>gb|AAF81710.1|AF250869-2
(AF250869) sulfonate monooxygenase
[Buttiiauxella sp. PNBS]"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83838.1"
/db-xref="GI:21956921"
/translation="MSINVFWFLPTHGDGHYLG
SEGARAVDYSYLQIAQAAADRLLGF
GGVLIPTGRSCEDSNLVAASLIPVTQRLKFLVAL
RPGNLTGGDPEELAAEGLHHLNHTERYEASAEEFT
HWWRKVLEGETVDFAGKHIQVKGA
KLLFPPVQHPRPFLYFGGSSAAAQDLAAEQUEVELY
LTWGEPPEQVKKEKIEEVRAAKAAK
GRTVRFGIRLHVIVRETTEAWRAANRLIANLDD
KTIADAQQQAFAGFDGSVQOQRMAAL
HGGKKDNLEISPNLWAGVGLVRGGAGTALVGDP
TVAQRIQEYADLGIDTFVFGYPH
LEEAYRVSELLFFPHLDLATTELPTQRPATQPQGE
VVANIYVPQKVQS"

gene complement (260746..2618 /gene="ssuA"
82)
CDS complement (260746..2618 /gene="ssuA"
82)
/locus-tag="y0245"
/function="transport of small
molecules; carbohydrates, organic
acids, alcohols"
/note="residues 18 to 333 of 378
are 73.10 pct identical to
residues 17 to 331 of 333 from E.
coli K12 : B0936; residues 18 to
333 of 378 are 73.41 pct identical
to residues 17 to 331 of 333 from
GenPept :
>gb|AAG55421.1|AE005283-8
(AE005283) orf, hypothetical
protein [Escherichia coli O157:H7
EDL933]"
/codon-start=1
/transl-table=11
/product="solute-binding
periplasmic protein of aliphatic

sulfonates, ABC transporter"
/protein-id="AAM83839.1"
/db-xref="GI:21956922"
/translation="MSLSFFFRRGFNVHRWLNIG
AMAAIITLAFTNTVIAQDNAPAOF
RIGYOKGSVNLVLAKTHQLLERKRPDTQISWIEF
PAGPQMLEALNVNSIDLGSTGDIP
PIFAQAAGADLILYVGMEPPPKPAEVILVPENSAI
NSVAELKGHKVAFQKGSSSHNLL
QALQKAGLKFDTIDQPVYLT PADARA AAFQQGNVDA
WVIWDPYYSALLQGGIRVLIDGS
QLNQTGSFYLASRPYTEANGPFIQVLEVLTQAD
ALTLSDRAQSI TLLANAMGLPEAV
IASYLDRHRPTAIQPLSQATVAAQQR TADLFFAN
RLLPVKVDISQRVWQFAGQLSSKP
PSSKPSSSKPSSSNQSSPSQLTDQPSIAQTSIE
QSSTAKSQTK"
gene complement (261897..2624 /locus-tag="y0246"
78)
CDS complement (261897..2624 /locus-tag="y0246"
78)
/note="residues 1 to 175 of 193
are 61.14 pct identical to
residues 1 to 175 of 191 from E.
coli K12 : B0937; residues 1 to
175 of 193 are 61.71 pct identical
to residues 1 to 175 of 191 from
GenPept : >dbj|BAB34443.1|
(AP002553) NAD(P)H-dependent FMN
reductase [Escherichia coli
O157:H7]"
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/db-xref="GI:21956923"
/translation="MRVISLAGSPRTPSRSAALL
NLSQHWLQQQNVEVIPYTLHDFQAA
DDLLRANFNSPDVSAFVAQLATA DGLLIATPIYK
ASFSGALKTLLDL PERALDHKKV
LPLATGGSIGHMLAVD YALKPVLTALKAQEVHLG
VFVDDSQVHVGEQVTVSTSATTR
LEEALESFYLALGRRKPLASNAVSSSLVQQTAA"
/locus-tag="y0247"
/locus-tag="y0247"
/function="enzyme"
/note="residues 9 to 225 of 233
are 34.10 pct identical to
residues 11 to 222 of 224 from
GenPept : >gb|AAB85318.1|
(AE000859) deoxyribose-phosphate
aldolase [Methanothermobacter
thermautotrophicus]"
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deoxyribose-phosphate aldolase"
/protein-id="AAM83841.1"
/db-xref="GI:21956924"
/translation="MIDFNDPRQVAKAIQFTNVN
ADLTREGVIKHLNICLEYQFDAAM
IAPCWVYLA KDVLKGSGVRVATTVNFPQANDTTA

MKVAIVRELAKEGADEFDFFPNPG
FLLGGLEDELYFNELKEVTHIAHDLGMVKAMLEF
GFITEEAMKIATRAYAEEAGIDWV
KQSSGWGKGGAATVEDVQLLKANIQAPCRVKVS
GKVNTLEKMKEMFLAGAELVGTSS
GPELVKGLTGDINAY"
/locus-tag="y0248"
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/function="enzyme; degradation of
small molecules; Carbon compounds"
/note="residues 4 to 299 of 310
are 39.26 pct identical to
residues 5 to 301 of 308 from
GenPept :
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(AE004621) ribokinase [Pseudomonas
aeruginosa]"
/codon-start=1
/transl-table=11
/product="putative ribokinase"
/protein-id="AAM83842.1"
/db-xref="GI:21956926"
/translation="MMSVFILGSYAKALVMTTDR
IPLAGETLIGYDFRQTWGKKGSDM
AVQAVRLGAEVAYAGVVGDDTFGHEFVGLMQEEG
VNIDALTISGELPTGAGLIVKDKE
ARNIVVDMGANKLFTPALVDSALSQLKQSNNVVL
TQLEIPLETARYGLQRAKEFGKIT
ILNPAPARDLRGLDLSAIDYLTPNETEARVALGL
PPDDPRSNREIANLLETCQYVV
MTLGESESSGSAVEGRNDTQEIPPC1IDVVDSNGAGD
SFNAALAVALDEGLPISEAVLFAN
ATAALCCMDWETVPSYRYREDVDAFMRSITVKEE
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/locus-tag="y0249"
/locus-tag="y0249"
/function="putative transport;
transport of small molecules;
carbohydrates, organic acids,
alcohols"
/note="residues 1 to 135 of 167
are 34.04 pct identical to
residues 1 to 139 of 139 from
GenPept : >gb|AAC22159.1| (U32732)
high affinity ribose transport
protein (rbsD) [Haemophilus
influenzae Rd]"
/codon-start=1
/transl-table=11
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permease"
/protein-id="AAM83843.1"
/db-xref="GI:21956927"
/translation="MRPDRIILHPELAAALATLGH
TDIILVTDAGFPIPPQAKRIDLGF
WPGTVDVLLHRLVRLKEIFVVEVRFASEVRDCHP
OLYRDVQTLYTGSQAEFOAQASHET
LCHDLAHQAKVVIRSGSFNPWANFALVASTDPFA
WFTDESGVKPLPAYVARQRILDN VVPELNA"
gene complement (265407..2663 /locus-tag="y0250"
48)
CDS complement (265407..2663 /locus-tag="y0250"

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/gene
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  /note="residues 54 to 306 of 313
  are 23.57 pct identical to
  residues 51 to 302 of 307 from
  GenPept :
  >gbi|AAG06959.1|AE004778-3
  (AE004778) transcriptional
  regulator MmsR [Pseudomonas
  aeruginosa]"
  /codon-start=1
  /transl-table=11
  /product="putative AraC-like
  regulator"
  /protein-id="AAM83844.1"
  /db-xref="GI:21956928"
  /translation="MACHDEPGYSLNFCHQHRVG
  RMEKNMQRTQVANWYRESDEFST
  LVNYRILRAGHIRAADNFHVRRQSVAGHELIFCL
  NGSGFIRLENNLHEVKGNGLAWLP
  VRWPHEHFVNKQEPWEILWLRIDGAKLNINIMQIL
  DVAQQPVFEFTSPETITDIYHRLF
  DLMQSHTLVADAHCDVLCSQLIYTLLLENRSFDAT
  KSPVISHRGLGRLIYQIHSHYND
  WDIDKFMOYCQVSKSQSLFRLFQETTFNQSPLRWLK
  NYRLSQARLLVETEETISRIAGL
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  RHD"
  /locus-tag="y0251"
  /locus-tag="y0251"
  /note="residues 18 to 370 of 376
  are 43.94 pct identical to
  residues 13 to 359 of 362 from
  GenPept : >dbj|BAB49039.1|
  (AP002998) hypothetical protein
  [Mesorhizobium loti]"
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  /transl-table=11
  /product="putative oxidoreductase"
  /protein-id="AAM83845.1"
  /db-xref="GI:21956929"
  /translation="MDTLLISQLEHATQPVLPKRR
  DYRIGIIGAGFIVECHCHLVAYQKA
  GFVPIGITSKEHSQNHRALETFAIKKVYETWQDM
  VCDPQIDIDIAVPPHIQLEIVRF
  ICESNSAAKHKIGILCQKPLAMSLKDGEIREVRLS
  QQSGIPIAVNSNMRYDPSMRALKY
  ILENQLIGDPVIASIDMRAIPDWQAFLQKYKKLE
  LYMAIIHHIDAFRFLFGDFVKVITA
  VCRTDPTTFFEHIDGITQYTFQYANGLIATSLD
  VWAWFGEPCAKNNYINWRVEGSDG
  LAEGDFGVHRRPEYCGSTLKLASRNHPGQWIAP
  KWERQWFPDAFIGTMANLMAIEE
  NRPPEISAEDNLGTLACIEACYLSIQQERTVYN
  EILLENAK"
  /locus-tag="y0252"
  /locus-tag="y0252"
  /note="endonuclease motif;
  residues 1 to 298 of 299 are 51.48
  pct identical to residues 1 to 303
  of 304 from GenPept :
  >dbj|BAB49038.1| (AP002998)

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unknown protein [Mesorhizobium loti]
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 /db-xref="GI:21956930"
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 KIKQAGMGCVQLDLEFTDIDLRRG
 RITKEKAHQVRNAFRRANIPIVAIASAYTNLVHPD
 PVKRAENIAAVKEILAHARHFGTP
 YVISETGTYNTDSWLYDFPKNSTEEAYQEFAIA
 KELATFAYEHHNAVFLEVENVNNI
 GSVGQVARLMQEVEHTRGLGLADPNTNYFDDKNID
 AIDETLHNIFNVLESRIKIAHAKD
 CKKTDAIAEKFGGGAAEHNFSRGAGSVELPAAGL
 GALNYPLVLELLAQKHPNIPLIIE
 HVDEEDIPRAKRFVDEVLMATGS"
 /locus-tag="y0253"
 /locus-tag="y0253"
 /codon-start=1
 /transl-table=11
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 /protein-id="AAM83847.1"
 /db-xref="GI:21956931"
 /translation="MDWIQDNSEMYLAGDWLTQT
 GLTG"
 gene complement(268916..2697 /locus-tag="y0254"
 10)
 CDS complement(268916..2697 /locus-tag="y0254"
 10)
 /note="residues 42 to 145 of 264
 are 31.77 pct identical to
 residues 163 to 258 of 325 from
 GenPept : >emb|CAB12673.1|
 (Z99108) similar to iron(III)
 dicitrate transport permease
 [Bacillus subtilis]"
 /codon-start=1
 /transl-table=11
 /product="hypothetical"
 /protein-id="AAM83848.1"
 /db-xref="GI:21956932"
 /translation="MCTAIAIYGTENIPPETAYE
 IGMLFFKVIELTISTGYYKYRED
 RSEEDIDFIEVSLSDLKNELKKNATSFRFYNES
 EKSNYWTASFGFSTSDFGGFYHFD
 AQCALSKNGKEFKFIEFIKEFSSKNNFSYGYIVNP
 DNVADGFYYAEGGNFVQIQYQYENP
 MFFEKEETGGMYEGQERYKNTMLRMVYPVNINHH
 HLDIIIGNVSLEKEWISSDEKHGT
 EGLNNDLWLWTVEDTKLDEVNKYLGEAGVLISWK
 PPTIKKAPRKLP"
 gene complement(269719..2742 /locus-tag="y0255"
 63)
 CDS complement(269719..2742 /locus-tag="y0255"
 63)
 /note="Rhs element associated;
 residues 89 to 1396 of 1514 are
 33.53 pct identical to residues
 112 to 1362 of 1517 from GenPept :
 >emb|CAD18288.1| (AL646083)

gene

putative RHS-related transmembrane protein [Ralstonia solanacearum]
/codon-start=1
/transl-table=11
/product="Rhs-like core protein"
/protein-id="AAM83849.1"
/db-xref="GI:21956933"
/translation="MFMTVAQSIGTGYGAAGAQSA
ALRQTAQGQQSPARTDYQVSNPNV
GNIARASDSLNVAESQQFNTLVTAGFGMQAIAA
GVAGGGVAKIGNKLGHGIARALN
FNQVATEGESPAHLGHPIAHQKKDWGVWGAIGGI
LLGAAAAALVVVTFTGJLVVIAAA
AAAAGLIGGIAAATGAALGQYGDNKGVIAEGSAN
VFFEGQPVARVGDKIQCSDPHSSP
PPMIAEGAKTVFANQKQIARLGHRTTCGNGINAG
CGSLAITQETAVYYEVADSRNPYL
RWSAVILSFLPIQKKFEQGFRSLKKPPNTAVNAT
HNCPTGSDPVDMVSGDYLQWPVI
DIAGVLVRLQRTYRSGDYFTVSGCFFGHKWADSW
SQHLVHEDNDIYIDEEGVGLSEF
TPENKVQAVNLYNLRYELVGERHGELEFRVDRSTQ
QTLHFNQQQQQQQRQLSAITDRKG
RIDFRYQQGELISVEHSMDGYVLEIDSRRHTIH
ELVTOEKRKQKLQSTFSERGYLVQ
CQSFQYGTLSHEYDPKGYMVRWRDTIDSTDVAVRY
DISGRVVALKTSTGFADHFIFYHD
KERYTIIYRDGEGETGYHYHNENNLLIKLVDPLGN
TTLTDWDLTQKIKETDALGRITRF
IYNERGDLTAVILPDETRETEYEYNPSGVVTAFTS
SAGDSWQYQYDRQGLLRQVTPSG
QTMSFRYGKGEVLRKIIAEDQWRYHYDHGCL
STIIDPKGNSTAVTLDVLGLRFLSH
QNALGEELTRYTHSDAHSFAGSVTKMMPDGVEQ
AIAYDSEKRIAALTDGAGKTTTRYE
YGGFDLTLGLIREPDGQRLTFGYDTLRLNQVTNA
SGDTYRYTRDRAGQVISETDFTG
TVHYQYDAVGRRIGARYPDQRLVRWHYSMQDQVL
AQQTWHCDALSSTLVGTVSYGYDG
AGRLLSATNADAVVEFDYDEAGQLVAERLNGREV
RHQWDALNTPVARQVGEGLGTFV
YGAQGEELTRLQLAGHQPLQLQHDRRLGRET
VRESAAGFIQACNYTPSGLLAHQAAGRNS
ALFQQQLIAPEPALHGSAVNRSWQYDRAYNVVG
MDDGRWGTQYQYDRNDQVVRADF
GGFLPLQE^QFSYDVNQNLREHRLCPRAQAVLAQ
ASQQQQAGRVVKRGDSQYRYDAAG
RLVEKRSQRDGYRQPQLWRYRWNEQDQLSELITPT
GARWRYGYDAFGRIRKLRVDTP
PLNEMDAPSTGPATASLAGYAYLWSDQQLIEEV
VYADGTVAYEQGIHNLAYAPGGLT
MARYAQGKLYHVYVADHLGTRRELLNEQGKVVWAS
RLSTWGQAEWLWQAANEEDRVSCN
LRFAGQYADAESGLHYNRFRYYDGETQYQLCPDP
IGLEGGLNPGYVHNPVSWDPLG
LATCPMRREVNGTKIFGKGQKDGTGHDQFSEVIA
NKLAMSGKFKEVYLNRSYNFANGK
GISGRRPDIMAVDMNGKVHAIELAS
KTDMGRKFPSLRTRNQDAMKNLPSIDRGSVIVL
EHQYNSKXK1NALDNLISGI"
complement (274302..2747 /locus-tag="y0256"
24)

CDS complement (274302..2747 /locus-tag="y0256"
24)
/note="residues 1 to 137 of 140
are 36.49 pct identical to
residues 4 to 140 of 143 from
GenPept : >emb|CAD18289.1|
(AL646083) conserved hypothetical
protein [Ralstonia solanacearum]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83850.1"
/db-xref="GI:21956934"
/translation="MYYFNEGSLELPEAWRDMTV
NVLTSSLDETVGLSFTVSRDTPPW
GMGFHEFFDREIGSLSRQLNHYQLLHQDTGEVNN
HPSVTAEECFWSSEQQRIHQMLMTLV
DIAPRVLILATMVGELETPOQKEHITAIVQTLQI
NARS"
gene complement (274727..2768 /locus-tag="y0257"
29)
CDS complement (274727..2768 /locus-tag="y0257"
29)
/note="Rhs element associated;
residues 77 to 696 of 700 are
46.91 pct identical to residues 3
to 633 of 633 from GenPept :
>gb|AAG54902.1|AE005236-3
(AE005236) Z0707 gene product
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="VgrG-like protein"
/protein-id="AAM83851.1"
/db-xref="GI:21956935"
/translation="MSGAQMTEMAGGIGDAVGGT
AGKRINQAAEVAKTALDAKAKVLD
GGVTPLNLAAAGGAGAGLPDSAAAALTRLVKQPSG
LQFTLTASLPPQTFAVVDFTLSE
MLSSPFVLNVGLASADPAVDFAAVLDEDATLFIW
REGVLRQRSITGMVASFEQGDTGFH
QTRYSMVIRPALWRTRSLRRNARIFQQASVEEIIIT
TLLKENGINDFAEFGFRHPHPVREF
CVQYQESDFDFIQQLTAEEGIFYFEFSAGKNTV
VYADDVGSLPKGASLYNPVNVAQ
AQELSITTFTRSAQVRPAMVQLKDYTFKNPWNAA
AFSEQSGELQNQRDPYEHFDFPGR
FKDAQHGQDFTRYRLDALRNDAHLGQGAANDFTL
QPQQLFLSFLYNHPRGDLNHAWQLLG
VQHSGKQMQALEQASGDQGTGVLFNHFSPFIPHTQT
WRPTFLAKPAMDGPQIAVMVGPPG
EEIYCXEYGRIRLQLFWDRYGGQSNNDNSSCWIRVT
QPWAQGQWGMALAPIRGQEVVVDF
LHGDPPDPQIVTGRTYHANNIPPGSLPASKTQMAF
RSKTHQGEGYNEMRFEDAKGGEGL
FMHAQKDMSTTVKDQNQTTTVEKGNNQTVTEVKGDR
TVTVATGNETTDITOGSLTETIKV
RRSTCANFIQVKAEGDAPGTQLYTATEQIKFVVG
KSSITLNPD\$IIQFSGSTSITLN
ANIDAIAPLINLNKDKG"
gene complement (276826..2769 /locus-tag="y0258"
24)

CDS complement (276826..2769 /locus-tag="y0258"
24)
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83852.1"
/db-xref="GI:21956936"
/translation="MFAHDKANNNKTA
DCKTGTVT
P THIVSPEAAQP"

gene complement (276946..2771 /locus-tag="y0259"
22)

CDS complement (276946..2771 /locus-tag="y0259"
22)
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83853.1"
/db-xref="GI:21956937"
/translation="MOTELNREIPL
EELLRLQAV
SADEHQAPASPVLI
KQIDDRWNALL
SRYHHLTQQTNSAR"
/locus-tag="y0260"
/locus-tag="y0260"
/function="regulator"
/note="residues 48 to 154 of 162
are 33.64 pct identical to
residues 6 to 108 of 112 from
GenPept : >gb|AAF94621.1|
(AE004224) transcriptional
repressor RstR [Vibrio cholerae]"
/codon-start=1
/transl-table=11
/product="transcriptional
repressor"
/protein-id="AAM83854.1"
/db-xref="GI:21956939"
/translation="MHRITISNSIAIRC
VFVFKS GLILEHLM
TDVIDEIMQTEEQRR
FGLRLKELRKQOHKTQKEVATRIGLQLSQYNKY
SGMHIP PADKLITLAELLVTSIDY
LLLGSNETSSIRNTRLERFK
ALSQCQPEE
QET
VILKIDAVIKHRV
ESALQFVDPE KK"
/locus-tag="y0261"
/locus-tag="y0261"
/note="residues 15 to 68 of 74 are
42.59 pct identical to residues 35
to 88 of 132 from GenPept :
>gb|AAA97244.1| (U14003) ORF-f132
[Escherichia coli]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83855.1"
/db-xref="GI:21956940"
/translation="MAKAHSTSGTG
INKTPKTER
YTYTGVYV
PQRGKRNP
PPAINLKG
WLEALGFFSGQ
PVLITEHGR
LVIQPEIKI"
gene complement (277977..2781 /locus-tag="y0262"
74)

CDS complement (277977..2781 /locus-tag="y0262"
74)
/codon-start=1

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|------|-------------------------|------------------------------------|
| | | /transl-table=11 |
| | | /product="hypothetical" |
| | | /protein-id="AAM83856.1" |
| | | /db-xref="GI:21956941" |
| | | /translation="MSHSPDRDSSPLSCIQAITI |
| | | LLYFKYCAGRKSCKNNIGFVDNEF |
| | | RDIIVHNTVENNIPHIIFISG" |
| gene | 278074..278265 | /locus-tag="y0263" |
| CDS | 278074..278265 | /locus-tag="y0263" |
| | | /note="residues 15 to 63 of 63 are |
| | | 34.69 pct identical to residues |
| | | 177 to 224 of 243 from GenPept : |
| | | >gb AAG55242.1 AE005267-7 |
| | | (AE005267) arginine 3rd transport |
| | | system periplasmic binding protein |
| | | [Escherichia coli O157:H7 EDL933]" |
| | | /codon-start=1 |
| | | /transl-table=11 |
| | | /product="hypothetical" |
| | | /protein-id="AAM83857.1" |
| | | /db-xref="GI:21956942" |
| | | /translation="MQDLRPAQYLKYNNIVMAWI |
| | | QDNGLSLSGEWLTQTGLTGQPLA |
| | | ISVMAGKVIIQFQKMNMLL" |
| gene | complement(278315..2788 | /locus-tag="y0264" |
| | 00) | |
| CDS | complement(278315..2788 | /locus-tag="y0264" |
| | 00) | |
| | | /note="residues 17 to 157 of 161 |
| | | are 25.97 pct identical to |
| | | residues 29 to 169 of 192 from |
| | | GenPept : >gb AAC12984.1 |
| | | (AF020713) unknown [Bacteriophage |
| | | SPBc2]" |
| | | /codon-start=1 |
| | | /transl-table=11 |
| | | /product="hypothetical" |
| | | /protein-id="AAM83858.1" |
| | | /db-xref="GI:21956943" |
| | | /translation="MKNPCQNCEKNIDLSDIKSV |
| | | EKTLYGSFPEAFVSHYLSFNGGPV |
| | | LRAWWACDDGCEPLEIAAFKPKFYHKMTNDNPNS |
| | | LIDGCYNEIMIRKNVIPSNIIPFGN |
| | | DWGGNFCLNKDDDSVVFYATDSFDPEVMSMKNH |
| | | DVLQKLTTSFEEFINGLVVEEDL E" |
| gene | complement(278802..2801 | /locus-tag="y0265" |
| | 72) | |
| CDS | complement(278802..2801 | /locus-tag="y0265" |
| | 72) | |
| | | /note="Rhs element associated; |
| | | residues 8 to 326 of 456 are 44.23 |
| | | pct identical to residues 957 to |
| | | 1250 of 1354 from GenPept : |
| | | >emb CAD08751.1 (AL627266) |
| | | Rhs-family protein [Salmonella |
| | | enterica subsp. enterica serovar |
| | | Typhi]" |
| | | /codon-start=1 |
| | | /transl-table=11 |
| | | /product="rhsD protein" |
| | | /protein-id="AAM83859.1" |
| | | /db-xref="GI:21956944" |

/translation="MAADLLPRQGDIWRKFSFD
 AGELSMATDIREGEQQYRYDAEGR
 LTDSEERHQLSVAEDFAYDNAADNLNLLNRKLPFD
 VDPLYDTPVANRNLQTQWQHYRFNEY
 DAWGNMTRRHAGGRMOMHFAYDDDNRLRLRAWGTGP
 LGEHDHSYRYDALGRRIHKSVTIK
 RGAETTTRQTDFIWQGLRLLQEQTDTGNATYIYD
 PNESYTPLARVDQRHGETESQVY
 FHTDINGTPLDVIDGEKGKHRWSGYHAWGKVTRQ
 NVSDPQRSTVSREAQPLRYPGQYS
 DDETGLHYNTFRYYDPEIGRFSTQDPIGLAGGIN
 LYQYGPNLWTIDPWGWAFFGVDF
 TGSPDLFPVKGSQNLIVETMQGARGRDFTEAFK
 LAGISKADATGYTWHHLNDFDPVS
 GKTIMQLVTTSAHEATFPHAGSVSQFEKHFNLP
 QSYGASADAIVASHSKWLGRIPK ALRSGC"
 gene complement (280200..2830 /locus-tag="y0266"
 91)
 CDS complement (280200..2830 /locus-tag="y0266"
 91)
 /note="Rhs element associated;
 residues 10 to 960 of 963 are
 37.73 pct identical to residues 1
 to 934 of 1364 from GenPept :
 >gb|AAI19248.1| (AE008708)
 putative RHS-family protein
 [Salmonella typhimurium LT2]"
 /codon-start=1
 /transl-table=11
 /product="Rhs-like protein"
 /protein-id="AAM83860.1"
 /db-xref="GI:21956945"
 /translation="MRRGPGRPAMFEARVDDKL
 YHSSALAGFIIGSIIAGAVIFAA
 AYAASIVLTGGATLVATGFIVGMGVTTLVVAGG
 LIRSVGEKIGSMCHHDVGQITTG
 KNVKVNSKRAAHVELSTVACKDOSAIQRMAGESS
 NIFINSKAAVRLLEDKTTCDAVVDS
 ASSNVTFGGGRVQYLDILKREISDEMRLSEKLF
 VAGLAGGIFGAAKQAGCFGLKCLS
 KIALGEMAGAAAGYGLEKGVGAIAGYFGYPVDVI
 SGQKLITGEGDDTDFILPGIFPLH
 WSRIYRSENHHVGALCQGWSLVWERSLRKEDDSI
 VYQNDEGREIVFPLIKRGERYFSP
 TEHIWLARTERDTYIASPFETCFIFEAFFSEAGV
 AKLASLEDLNIGHALYFSYDDIGOL
 KKISTTSGYGVYCQYEKGRLVSVACVKGGTPGTL
 VRYQYNEQHQLVSVTNREGQITRQ
 FGYGHHLINKLADVRGLECRYTWADIGGTPRITH
 SATNLGEQWQFYDIDNQQTTLTD
 LNTGQTAWCGYNAQHLITDYRDFDGKYAFDYN
 LNMPVRRVLAGERTLVLVYDALAR
 PIQITDPLKRETHIDYHRNSLRVVRQYPDGQVW
 KGEYDRTGRLLKENAPDGGVTLYH
 YPGASSLPERITNAVGQATHLGWERHGQLTETD
 CGSKLTRYEYDIDGHLTLVIDAEN
 HSTHYSYNRLGOPTGIRYADGRKEOLRYNAQGLV
 EQFTDPVGRQLHWRYNLRQGPVFS
 TDRLQREYRYRDCHGQMIELDNANGGQYHFRWS
 SGGQLVVEQYPDNLVRYRYRGEKG
 MLMALETTAPTVDDLTIVSRQVSFEDYDAGGRMTQR
 LTGMSATRYDWIDMORLLAERVP

TAVGEQAGIVGHGVRLAYDKAGHLLTESGDLGAV
TYQWDPLHHLAALTLFDGTLWSL
RYGAGHVSIAIRHGDTLISEFSRDNLHREVSRVTQG
ILTQYRDYDAMGRRL"

gene complement (283057..2835 /locus-tag="y0267"
15)
CDS complement (283057..2835 /locus-tag="y0267"
15)
/note="residues 9 to 144 of 152
are 35.71 pct identical to
residues 5 to 144 of 148 from
GenPept : >gb|AAL19247.1|
(AE008708) putative cytoplasmic
protein [Salmonella typhimurium
LT2]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83861.1"
/db-xref="GI:21956946"
/translation="MPENNINTNYC1QEGTLECP
GFTDRTVNLFMKGKPGAAFALNIA
RDVPEAQHVSIAIRHGDTLISEFSRDNLHREV
QIDVGAQHPIPGEYVEATYMAETRR
VWQRQVAIQVGDHMMIFTATNASPFNPQQQATWE
QWIHSFAWPWAREAGHV"
gene complement (283521..2859 /locus-tag="y0268"
23)
CDS complement (283521..2859 /locus-tag="y0268"
23)
/note="VgrG-like protein (Rhs
element associated); residues 169
to 792 of 800 are 44.06 pct
identical to residues 3 to 674 of
713 from GenPept : >gb|AAC62387.1|
(AF044506) VgrG protein
[Escherichia coli]"
/codon-start=1
/transl-table=11
/product="VgrG-like protein"
/protein-id="AAM83862.1"
/db-xref="GI:21956947"
/translation="MFAHDKANNKAADKTGT
VTPHIVSPEAAPTVSGAQMT
IGDAVGGTAGKRINQAAEVAKTALDAKAKVLDGG
VTPTNIVATGPAPTVSGAQMT
GGIGDAVGGTAGKRINQAAEVAKTALEAKAKVLD
GGVTPMNLAAAGGAGAGLPDSAAA
ISRLVKQFSGLQFTLTTASLPPQTFAVVDFTLSE
MLSSPFVLNVGLASADPAVDFAAV
LDEDATLFIWREGVLRQSITGMVASFEQGDGFH
QTRYSMVIRPALWRSTSLLRNARIF
QQASVEEIITLLKENGINDFAFGFRPHPVREF
CVQYQESDFDPIQLTAAEFIGFY
FEFSAGKNTVVYADDVGSLPKGASLPYNPNVAAQ
AQELSITTFTRSAQVRPAMVQLKD
YTFKNPNWAAAFSEQSGELQNQRPDYEHFDFPGR
FKDAQHGQDFTRYRLDALRNNDANL
GQGASNDFTLQPGQQLFSLYNHPRGDLNHAWQLLG
IQLHSGKQMQALEQASGDDQGTVLFN
HFSFIPHTQTWRPTFLAKPAMDGPQIAMVVGPPG
EEIYCDEYGRIRLQFLWDRYGQSN

DNSSCWIRVTQPWAGQGWGMLAIPRIGQEVVVF
LHGDPDPQPIVTGRTYHANNIPPGS
LPASKTQMFRSKTHKGEGYNEMRFDEAKGEGL
FMHAQKDMMTMVNLNDRKTDTQDH
SEHIGQDQSNTVVRNQSNNTIQNDRVEVTRDQQT
EVGNDYQLVVKGEKKFVTKIRYT
EVHEDETILTVTKS1KIHAKQGDIS1STPNAGITI
THDGAIVLQGKYIIRLAADMIDLNP EE"
gene complement (285945..2872
57) /locus-tag="y0269"
/note="disrupted by frameshift"
/pseudo
gene 287229..287591
CDS 287229..287591 /locus-tag="y0270"
/note="residues 19 to 79 of 120
are 34.84 pct identical to
residues 53 to 114 of 311 from
GenPept : >gb|AAC17095.1|
(AC004482) hypothetical protein
[Arabidopsis thaliana]"
/codon-start=1
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/product="hypothetical"
/protein-id="AAM83863.1"
/db-xref="GI:21956948"
/translation="MMICCGVSLMQTHPLIVFLP
PKQQEDVMTTINTICLNASVSMRS
VSIQSCVSIQSVWQTEFTETQTAREWVVGIFINKDA
VRHLAAINLEADIEGVGAHIGQFT
GVDQFPQLRPRTEAEGAR"
gene complement (287382..2908
42) /locus-tag="y0271"
/note="disrupted by frameshift"
/pseudo
gene complement (290946..2923
52)
CDS complement (290946..2923 /locus-tag="y0272"
52) /note="residues 213 to 462 of 468
are 53.33 pct identical to
residues 8 to 259 of 264 from
GenPept :
>gb|AAG54520.1|AE005198-1
(AE005198) Z0251 gene product
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
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/product="hypothetical"
/protein-id="AAM83864.1"
/db-xref="GI:21956950"
/translation="MSLVRHMDITSQHFWHVLLQ
APLSPEQTAQALADDPPQWEYIDG
QMVKLGSLAHATLNNIDDIOQQAMALLSQSKDFR
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LTEYVQLFWTTAWPQNPLHKRRFAQQQILKRFDSA
SSSFSSQRADAQRENVQGGLLAHLA
OVWHSHREPLGAKEVDALRSRYARPVERVIEAVAS
DEPLSSNTLAAAMAATPVSPSLAI
DNTSDRAWRQTLKMDALLSEQQPDAAIIGFRLRR
HAVWGAUTAPPMAQSDGRTPLAAV
SADRATADYLARLANADLPLWHQVEQSLSLTALPYWL
DGHVLSAQIALQLGYDAVAQAIRD

ELSVFLARIPALKTLFFTDMDTPFLSSSESAAWLQQ
DANHQGRSRSTIEQDEIWIWCYQQGG
LEAALQMNRQPOQSERPRDRFYHQQLLSAQLFKEA
GLTALAQQHYSLLVGQQLQLSE
WEPA利亚TEQRQLKP"

gene complement (292340..2930 /locus-tag="y0273"
35)
CDS complement (292340..2930 /locus-tag="y0273"
35)
/note="residues 36 to 231 of 231
are 50.00 pct identical to
residues 47 to 244 of 247 from
GenPept :
>gb|AAG54522.1|AE005198-3
(AE005198) Z0253 gene product
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83865.1"
/db-xref="GI:21956951"
/translation="MFAMNTWLLISSLFSGGHT
DAFWTMGLPPPVAEKEEAGTALAV
MRCRSENSALVRLCDYDKALSPVNADEVKRVNAG
PAWQRANQEKGRTDHSTAFLVTE
GEGSNPMLITTPAIGMPPEPRVLMSCIDNITR
LQIALVGVPQKESSVTLLIDKAGII
DKTRLDAQWFRLRENGYLLESSRLLAGIDEIKRML
SAETLTIEGANGAFPRLTFTLSQL
TPALKPLRNACHW"
gene complement (293023..2938 /locus-tag="y0274"
20)
CDS complement (293023..2938 /locus-tag="y0274"
20)
/note="residues 194 to 260 of 265
are 29.57 pct identical to
residues 454 to 524 of 530 from
GenPept : >gb|AAF96031.1|
(AE004353) sigma-54 dependent
transcriptional regulator [Vibrio
cholerae]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83866.1"
/db-xref="GI:21956952"
/translation="MRQRLLKSVLALLDNNDSTEQL
IHRFLTINHHHRQRFSALMVSMFNA
SEGRLCDYHQPDGGMNVALKLDANIEDVNHPFLVR
VLRNGFPPEWGSLYQGVRIEDDDF
RSFIQALPTRCGLYALPLFDVHGHAACVIAVFSE
NIERFADTRGIFSIVCHIQHRLN
KLQEMDQLRSQFNQIRTVFKEQRQREKQLDELLV
SLSTSDDHALPGISQDYSKIDSLSLT
TAVETFECAVLTQRQLYGNDSRIAASLGLSLR
ALTYKLAKYRQCL"
gene complement (293817..2964 /gene="clpB"
20)
CDS complement (293817..2964 /gene="clpB"
20)
/locus-tag="y0275"
/locus-tag="y0275"

| | |
|------|---|
| | /function="putative enzyme;
degradation of proteins, peptides,
glyco"
/note="residues 153 to 857 of 867
are 40.22 pct identical to
residues 133 to 849 of 857 from E.
coli K12 : B2592; residues 1 to
866 of 867 are 67.25 pct identical
to residues 1 to 910 of 923 from
GenPept :
>gb AAG54523.1 AE005198-4
(AE005198) putative protease
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="heat shock protein"
/protein-id="AAM83867.1"
/db-xref="GI:21956953"
/translation="M I Q I D L P T L V N R L N P I A R H S
L E A A A A H C V S Q Q E A E I T V S Q V L L Q
M I S T P L C D V R L I L S H A G V E E D E L R E S L D Q R V S G Y
Q A I T Q A Y P S F S P L L V E W L Q D S W L L
A S T E M H S Q L R S G V M L L T L L S P S R Y L V P T A N R L
L S P I N R E L L R Q N F A N W T A D A E T P
R A E K G A E A N G A E I N G D S L L A R Y A S N M T E Q A R N G
E L D P V L C R D T E I D L M I D I L C R R K
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G L D I S N L L K P A L A R G E L K T I A T T
W S E Y K K Y F E K D A A L S R F Q L V K V S E P S A Q E A T I I
M R G L R T V Y E Q A H G V L I D D E A L Q A A
A V L S D R Y I S G R Q L P D K A I D V L D T A A R V A I N L T S
A P R Q V S A L K N E L Y H Q G M E I E M L E R
E Q R L S L S R P D E R L S V L Q Q Q R I E I E Q Q L I A N T G W
E K Q Q H V L V Q Q I I A L R A V L L A Q E E S A
T D E Q V V N L T A L S D E L E R L Q Q H Q T L V S P H V D K S Q I
A A V I A E W T G V P L N R L S Q S E L A V V T
E L P S Y L G Q O I K Q O E T A I H C L H Q H L L T A R A D L R P P
G R P M G A F I L V G P S G V G K T E T V L Q I
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D E V E K A H P D V L N L F Y Q A F D K G E L A D G E R I I D C K
N I V F F L T S N L G Y Q T I V D H A D E P A L
L N E R L Y P E L S A F F K P A L L A R M E V V P Y L P L G M E T L
Q I I I H G K L N R L D T L L R Q R F S A D V V
I E P E V I D E I L L R A T R A E N G A R M L E S I I D G A L L P P
V S L L L Q K V A A G T A I S H I R I A V E G
N V F T A Q V E G A I " |
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| CDS | 98)
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98)
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residues 18 to 252 of 253 from
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[Escherichia coli O157:H7 EDL933]"
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LGHGWNTQNGLWQSLLVHFHNETWGGEKVVLL
ERLMGEPKRYQDLLEFIYLFCFLG
YRGRYKVTSQNGDDEFERLFRLRHQQLQRLRGDAP
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LLS"
gene complement(297198..2985 /locus-tag="y0277"
44)
CDS complement(297198..2985 /locus-tag="y0277"
44)
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TLSVSTQLKGFMDEVEGTLVERAQ
LLAKRIGSPGQQGQIADVAEFMMLQVFNRNTQPLFT
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RTFTIDESRLLAGTFPVYHNHDLTDSFQPLFLAMRQ
ALSTVLTTPRAISIQLHMQAHGIRV
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TKITSLEKIRDVLVSQVLPGVPLVA
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gene complement(298547..2990 /locus-tag="y0278"
92)
CDS complement(298547..2990 /locus-tag="y0278"
92)
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gene complement(299092..3004 /locus-tag="y0279"
08)
CDS complement(299092..3004 /locus-tag="y0279"
08)
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PLMRGFDQQLPIRNQSEAHDFLEE
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gene complement(300534..3016 /locus-tag="y0280"
31)
CDS complement(300534..3016 /locus-tag="y0280"
31)
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 SKMLAYAGLLASPGRAPEVICSLV
 SHCFLNLPDITLHSWQLRKVDIAPSQQNRGLTRVK
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 RSGKFLLCINKLTREQFELSPFLPNCANYASLVMFV
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 58)
CDS complement (301586..3024 /locus-tag="y0281"
 58)
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 [Vibrio cholerae]"
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 AEENVSVSLLTCTNRELPLSLRVGDIQLSTDSPS
 FATFRNITRPSVPLYPVLDGGLHW
 SLLSNMSLNYMSLLDKDALQILHTYDFPSLHNR
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 FRGLPVRGLQTTLWLEQQGAFSSEGEYLFLSTVLA
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gene 302218..302895
CDS 302218..302895
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 related functions"
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 residues 56 to 224 of 226 are
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 [Escherichia coli]"
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 AGLEHHLSSRTYTPEFRLCVVRYMMANRCSAADAS
 AHFNIPNETIIQNWMKRYREGGKE
 ALNPSKTGTMPKDYEHDSPKFSEMTAHELEKE
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repeat-region 302324..303509
gene 302949..303569
CDS 302949..303569
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 related functions"

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207 of 283 from GenPept :
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/function="IS and transposon
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identical to residues 1 to 340 of
340 from GenPept : >gb|AAC13168.1|
(AF053947) putative transposase
[Yersinia pestis]"
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SLSVPQEPEPAVRFETEPGRQMQVWDGTMNRNGRS
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YDTLETCHRNAFRFFGGVPREVLYDNMKTVVLQR
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PRLCRPFRAQTKGVERMVQYTRNSFYIPLMTRL
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/function="IS and transposon
related functions"
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identical to residues 1 to 260 of
260 from GenPept : >gb|AAC69770.1|
(AF074612) putative transposase
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NENIVLGPSPGVGKTHLAIAMGYEAVRAGIKVRF
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RGVMAPRLLIIDEIGYLPLFSQEEAKLFFFQVIAKR
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VIAEANPE"
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63)
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24)
CDS complement(305910..3080 /locus-tag="y0286"
24)
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transport of small molecules;
cations"
                                /note="similar to colicin V
secretion ATP-binding protein
CvaB; residues 1 to 698 of 704 are
57.16 pct identical to residues 1
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[Klebsiella pneumoniae]"
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ATPase"
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VPQVLQTEAAECGLACLVMTCRYH
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MSHFVVLVAVKGTREIIHDPAFGRRTVSLSEMSQ
HTGVALELWPNSEFTRQKSRTL
SLLSLMRNISGLPGFLTKIFCLSLMVEAINLLP
VGTQLVMDHTVIIAEODYDLLALICI
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DCIAVCLQDDKLFLAGSIADNIASFVNKEQRIL
SCANHNCNHLKEIMHMMPMGYETLIS
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gene complement(308017..3093 /locus-tag="y0287"
33)
CDS complement(308017..3093 /locus-tag="y0287"

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transport of small molecules;
cations"
/note="similar to colicin V
secretion protein CvaA; residues
14 to 438 of 438 are 47.05 pct
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424 from GenPept :
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protein [Escherichia coli]"
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GLITKDQLTNQRSLFYQQQNAFQS
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FQKGDLKRQLAEVDASGMLLINSF
SDGKIENNSVTQGQMVNNDLSVQLTSPSDNPYYC
LVLWVPNNNSVPYINTDKVNIRYD
AEPFEKFQOFPGRIISISNVPVVSQQEIASYNIAP
RLPNGLIEPYKKVIVALDDIHF
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DIKKSVTGPVNE" |
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| CDS | 309522..309761 | /note="residues 12 to 72 of 79 are
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383 to 440 of 657 from GenPept :
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[Bacteriophage rlt]"
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| CDS | 309936..310085 | /note="residues 7 to 48 of 49 are
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262 to 303 of 355 from GenPept :
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[Caenorhabditis elegans]"
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gene complement (310351..3105 /locus-tag="y0290"
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complement (310351..3105 /locus-tag="y0290"
12)
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159 to 195 of 195 from GenPept :
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sylvatica]"
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GenPept : >gb|AAG31016.1|
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protein D [Lycopersicon
esculentum]"
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CDS complement (311092..3115 /gene="menG"
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carriers: Menaqinone, ubiquinone"
/note="menaquinone biosynthesis;
residues 1 to 161 of 161 are 87.57
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of 161 from E. coli K12 : B3929"
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CDS complement (311719..3126 /gene="menA"
 48)
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 308 from *E. coli* K12 : B3930;
 residues 12 to 309 of 309 are
 69.12 pct identical to residues 8
 to 305 of 309 from GenPept :
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 octaprenyltransferase [*Salmonella*
 typhimurium LT2]"
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 octaprenyltransferase"
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 GLLATAVLNINNLRDIENDKANGK
 NTLAVRLGPVVARYYHALLIGAAIFCLALFSILH
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 03)
CDS complement (312872..3142 /gene="hsuU"
 03)
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 /note="homologous to chaperones;
 residues 1 to 443 of 443 are 90.29
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 of 443 from *E. coli* K12 : B3931"
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 ATPase subunit"
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KEALKLIIEEEAAKLVNPEELKQQAIDAVEQHGI
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VQRDLPLVEGCTVSTKHGMVKTDHILFIASGAF
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LTTDDFERILTEPSASLTEQYKALMATEGVTIIEF
TREGIRKIAEAAWQVNERTENIGA
RRLHTVLERLMDISYDASESSQSQSITIDAEGYVG
KHLDELVADEDLSRFIL"
gene complement(314274..3147 /gene="hslV"
98)
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98)
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    /function="enzyme; degradation of
proteins, peptides, glyco"
    /note="residues 1 to 174 of 174
are 90.80 pct identical to
residues 1 to 174 of 176 from E.
coli K12 : B3932; residues 1 to
174 of 174 are 100.00 pct
identical to residues 1 to 174 of
174 from GenPept :
>emb|CAC88971.1| (AJ414141) heat
shock protein [Yersinia pestis]"
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proteasome-related peptidase
subunit"
/protein-id="AAM83887.1"
/db-xref="GI:21956974"
/translation="MTTIVSVRRDGHVVIGGDGQ
VTLGNNTVMKGNAKKVVRLLYNNKVI
AGFAGGTADAFTLFELFERKLEMHQGHLTKAAVE
LAKDWRTDRMLRKLEALLAVADET
ASLIIITGNGDVQVQPEDDLIAIGSGGPyAQSAARA
LLENTELGARDIVEKSLSIAGDIC
IYTNRQFTIEELTY"
gene complement(314898..3157 /gene="ftsN"
43)
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CDS complement(314898..3157 /gene="ftsN"
43)
    /locus-tag="y0296"
    /function="phenotype; cell
division"
    /note="residues 1 to 281 of 281
are 49.68 pct identical to
residues 1 to 319 of 319 from E.
coli K12 : B3933; residues 1 to
281 of 281 are 51.38 pct identical
to residues 1 to 324 of 324 from
GenPept : >gb|AAL22933.1|
(AE008891) essential cell division
protein [Salmonella typhimurium
LT2]"

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protein"
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/db-xref="GI:21956975"
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RKKRSAPIVSKTVMALAVALLVVF
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ERWRYIKELENRQIGVPMPTEPSA
GGEVNAKTELNEQRQLLEQMADMRQQPTQLSE
VPYNQGMQQVPRSAVTIKEPFATSV
QPQPVTPPRQTTPVQPAQAPVRTPAAAPVTQA
VTPPKVEKEKEKTQRWMVOCGSFK
AVDQAESIRALQAFAGIESRITSGGGWNRVVLGP
YNSKAADAKALQRLQGAGQSGCIP LSVGG"
gene complement(315809..3168 /gene="cytR"
37)
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CDS complement(315809..3168 /gene="cytR"
37)
/locus-tag="y0297"
/function="regulator; global
regulatory functions"
/note="residues 1 to 339 of 342
are 71.38 pct identical to
residues 1 to 339 of 341 from E.
coli K12 : B3934"
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/transl-table=11
/product="regulator for deo
operon, udp, cdd, tsx, nupC, and
nupG"
/protein-id="AAM83889.1"
/db-xref="GI:21956976"
/translation="MENKKETMTTMKDVAEMAG
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GDCAQQTQQERTFVNLIITKQIDGMLLGSNLFP
DASKEEQRNLPPMVMANEFAPELE
LPTVHIDNLTAAYEAVNYLHELGHKRIACIAGPE
SLPLSHYRLQQYIQLRNRNGITVD
NDYIIRGDFSYEAGAQSFALMELPHFPTAIFSH
NDVMAVGAIWQAKQLGLRIPQDVS
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LLEQLQGHQSRSRLLDETEIIR ESTAAPKH"
gene complement(317190..3193 /gene="priA"
88)
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CDS complement(317190..3193 /gene="priA"
88)
/locus-tag="y0298"
/function="factor; DNA -
replication, repair,
restriction/modification"
/note="factor Y; putative
helicase; residues 1 to 731 of 732
are 73.08 pct identical to
residues 1 to 731 of 732 from E.
coli K12 : B3935; residues 1 to
731 of 732 are 72.67 pct identical

```

to residues 1 to 731 of 732 from
 GenPept : >gb|AAL22935.1|
 (AE008891) primosomal protein N'
 (= factor Y) directs replication
 fork assembly at D-loops
 [Salmonella typhimurium LT2]
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 /db-xref="GI:21956978"
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 RILCWATETYHYPIGEVLFHALPI
 LLRQGRPAQSAPLWQWFVTEQGRATPPESLKRAP
 KQQQALAAALLKQPVYRHQNEMAL
 TESALQALRSKGLIDLRAQEATTDRHSFSVLG
 ERRLRNTEQATAVGAIRSEDNQFA
 AWLLAGVTGSGKTEVYLSVLENILAQGRQALILV
 PEIGLTPQTIAFRERFNAPVEVL
 HSGLNDSERLSVWLRARSGEAAIVIGTRSLFTP
 FSRLGVIIIDEEHHDSSYKQQEGWR
 YHARDLAVFRAREEGIPIVMTATPALETLHNVQ
 MGKYRQLTLTKRAGSAKPAAOHLL
 DLKGLPLKVGLSQPLLKQMKTHLQAGNQVILFLN
 RRGYAPALLCHECGWIAECQRCDH
 YYTLHQNHRLQRCHHCDSPRPVQQCPKCGSTHL
 VSVGVTQELENELAPLFPEPTPIT
 RIDRTTSRKGSLEQYLADVHQGGARIILGTQML
 AKGHHHFPDVTIALLVDGALFSA
 DFRSAERFAQLYTQVSGRAGRACKQGEVILQTHH
 PEHPLLQILLQGYDAFAKQALEE
 RKSVFLLPYTSIIIVRSEDHDNQOSALFLQQLRN
 LLEASPLKDEALWIMGPVPALQAK
 RGGFRFWQLLQHPSRQLLQRLIKTSQPLISTLP
 QARKVKWTIDVDPID"

| | | |
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/locus-tag="y0299" |
| CDS | 319574..319846 | /gene="rpmE"
/locus-tag="y0299"
/function="structural component;
ribosomal proteins - synthesis,
modification"
/note="residues 20 to 89 of 90 are
81.42 pct identical to residues 1
to 70 of 70 from E. coli K12 :
B3936"
/codon-start=1
/transl-table=11
/product="50S ribosomal subunit
protein L31"
/protein-id="AAM83891.1"
/db-xref="GI:21956979"
/translation="MWCLAEQGWIA TRPNIEVSM
KQGIIHPKYEQVTASCSCGNVIKIN
STVGHDLNLDVCGECHPFYTGKQRDVASGGRVDR
FNKRKFVSPGAKK" |
| gene | complement (320371..3208 | /locus-tag="y0300"
38) |
| CDS | complement (320371..3208 | /locus-tag="y0300"
38) |

/note="residues 13 to 140 of 155
are 65.62 pct identical to
residues 10 to 137 of 146 from E.
coli K12 : B3562; residues 5 to
150 of 155 are 57.53 pct identical
to residues 1 to 146 of 166 from
GenPept : >emb|CAD13669.1|
(AL646057) hypothetical
transmembrane protein [Ralstonia
solanacearum]"
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LALESKEGYFGVTFMFMLFGIAVQKNTRDSAMSS
DTEASASLFKVRDQLKAED"
gene complement(321175..3214 /gene="metJ"
92)
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CDS complement(321175..3214 /gene="metJ"
92)
/locus-tag="y0301"
/function="regulator; amino acid
biosynthesis: Methionine"
/note="residues 1 to 105 of 105
are 89.52 pct identical to
residues 1 to 105 of 105 from E.
coli K12 : B3938; residues 1 to
105 of 105 are 91.42 pct identical
to residues 1 to 105 of 105 from
GenPept : >gb|AAL22939.1|
(AE008891) transcriptional
repressor of all met genes but
metF (MetJ family) [Salmonella
typhimurium LT2]"
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genes but metF"
/protein-id="AAM83893.1"
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KERSDEIPEAAKILMRELGVDPDT WEY"
gene 321789..323029
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/note="metB; disrupted by
frameshift"
/pseudo
/gene="metL"
/locus-tag="y0303"
gene 323032..325467
/locus-tag="y0303"
/function="enzyme; amino acid
biosynthesis: Methionine"
/note="residues 8 to 811 of 811
are 83.95 pct identical to
CDS 323032..325467

residues 7 to 810 of 810 from E.
 coli K12 : B3940; residues 8 to
 811 of 811 are 83.95 pct identical
 to residues 7 to 810 of 810 from
 GenPept :
 >gb|AAG59141.1|AE005625-4
 (AE005625) aspartokinase II and
 homoserine dehydrogenase II
 [Escherichia coli O157:H7 EDL933] "
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 homoserine dehydrogenase II"
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 FIHDLERLAGLDDNNIKDDVVIYAAEVVGHGHEIWSAR
 LMSALLNKLMDMAVLDARFLRA
 ERAAQPQIDESRSYPLLQQQLMAQPHQRLVVTGF
 ISRNNEAGETVLLGRNGNSDYSATQV
 GALGAERVTIWSDVAGVVSADPRKVKDACLPLP
 LRLDEASELARLAAPVLHTRTLQP
 VSGSDIDLQLRCSYQFEQGSTRIERVLASGLGAK
 IVTSHDDVCLIELQIASSHDFSLA
 QKEIDLKKRAQIKPLATGIGHPDRNLLQLCYTSE
 VVNALSRLVLEDAALPGKLSLREGL
 ALVALVGAGVSKNPFLSHRFYQQLKDQPVFVFVWQ
 AEDGISMVAVRLRGFTELHLIQQLH
 QSLFRAEKRIGLMFLGKGNIIGARWLELFAREQKS
 LSARSGFEFVLAGVVDSRSLLSY
 DGLDASRTLAFYNDNEAKEQDEESFLWMRRAHPFD
 DLVVLVDVTASP SLAEQYLDFAASYG
 FHVISANKLAGASSNNYRQIRDRAFTGRHWLY
 NATVGAGLPVNHTVDRLDRGDSI
 LAISGIFSGTLSWLFQFDGSVPFTELVDQAWQQ
 GLTEPDPRVDSLGSQDVMRKLVILA
 REAGYDIEPNQVRVESLVPAGAEGSGVQDFFENG
 EALNQQMQLRLEAAKEMGLVLRVY
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 /locus-tag="y0304"
 /function="enzyme; central
 intermediary metabolism: Pool,
 multipurpose conversions"
 /note="residues 1 to 294 of 294
 are 86.39 pct identical to
 residues 1 to 294 of 296 from E.
 coli K12 : B3941; residues 1 to
 294 of 294 are 91.83 pct identical
 to residues 1 to 294 of 298 from
 GenPept : >gb|AAC72242.1| (U74302)
 5,10-methylenetetrahydrofolate
 reductase [Pectobacterium
 carotovorum]"
 /codon-start=1

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folate reductase"
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GLLKDVGDFDISVAAYPEIHPEAK
SAQADLNLKRRKIDAGANRAITQFFFDVESYLRF
RDRCVATGIDVEIVPGILPVSNEFK
QLQRFAATMTNVRVNPWNMTSIFDGLDNDPETRKMV
GASVAMDVMVKILSREGVKDFHFYT
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repeat-region complement(326721..3281 /note="insertion element"
72)
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gene complement(326762..3273 /locus-tag="y0305"
61)
CDS complement(326762..3273 /locus-tag="y0305"
61)
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related functions"
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residues 1 to 198 of 199 are 54.54
pct identical to residues 41 to
238 of 240 from GenPept :
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[Escherichia coli]"
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gene complement(327602..3282 /locus-tag="y0306"
43)
CDS complement(327602..3282 /locus-tag="y0306"
43)
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related functions"
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residues 43 to 211 of 213 are
39.64 pct identical to residues 1
to 167 of 173 from GenPept :
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[Escherichia coli]"
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 32.30 pct identical to residues
 328 to 389 of 550 from GenPept :
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 [Agrobacterium tumefaciens]"
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 55)
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 CDS complement (328859..3315 /gene="ppc"
 55)
 /locus-tag="y0308"
 /function="enzyme; energy
 metabolism, carbon: Fermentation"
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 are 82.10 pct identical to
 residues 1 to 883 of 883 from E.
 coli K12 : B3956; residues 21 to
 898 of 898 are 82.10 pct identical
 to residues 1 to 883 of 883 from
 GenPept : >dbj|BAB38308.1|
 (AP002567) phosphoenolpyruvate
 carboxylase [Escherichia coli
 O157:H7]"
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 carboxylase"
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 ITRRTLHKLVEVNNTCLSQLDHNNDLADYERNKIM
 RRLROLVAQSWSHTDEIRKLRPSPV
 DEAKWGFAVVENSLWEGVPAFLREFNEQLENSDL
 YRLPVEAIPRTSWMGGRDGNP
 NVTAEITRHVLLLSRWKATDLFLRDIOVLVSELS
 MSECTPRELAGGEEVLEPYRQL
 MKNVRTQLNTQAYLEARLKGERVLPPHDLLVSN
 DQLWEPLYACYQSLSKACGMIEIAN
 GQLLDTLRVRVRCFGVPLVRI DVRQESTRHTDAIA
 ELTRYLGLGYESWSESDKQAFLV

RELNSKRPLVPLKWEPSAETQEVLTCRVIAEAP
 QGSIAAYVISMALKVPSDVLAVHLL
 LKEAGCPFTLPVAPLFETLDDLNNAADDVMTQLLG
 IDWYRGLIQQGKQMVMIIGYSDSAKD
 AGVMAASWAQYRAQDALIKTCEKAGITLTLFHGR
 GGSIGRRGGAPAHAAALLSQPPGSLK
 GGLRVTEQGEMIRFKFGLPEVTISSLALYAGAIL
 EANLLPPPEPKKEWIEVM DLLSDA
 SCDMYSRSVRENPEFVRYFRAATPELELGKLPLG
 SRPAKRRPDPGGVESLRAPWIFAW
 TQNRLMLPAWLGAAGLAGLQRRAIDAGKQDVLATMCR
 DWPFESTRIGMLEMVFAKADLWLA
 EYYDORLVDKSLWPLQOQLRDQLAADIKVVLIA
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gene complement (331869..3330 /gene="argE"
 38) /locus-tag="y0309"

CDS complement (331869..3330 /gene="argE"
 38) /locus-tag="y0309"
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 biosynthesis: Arginine"
 /note="residues 1 to 386 of 389
 are 77.72 pct identical to
 residues 1 to 381 of 383 from *E.*
coli K12 : B3957"
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 deacetylase"
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 DLGFRVEIQPVDPDTRHKFNLLASIGENENGEGHG
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 LTKPLYILATADEETTMAGARYFA
 ANTQLRPDFAIIGEPTSLQPVRAHKGHISNAIRI
 TGQSGHSSDPARGVNAIDLHESI
 TQLMALRTTLQERYHNPFAFTIPYPTMFNGHINGG
 DAANRICACCELHMDIRPLPGLTL
 SDNLNELMTEALEPVSQRWPGRLSDELHPPIPGY
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gene 333283..334287 /gene="argC"
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CDS 333283..334287 /gene="argC"
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 biosynthesis: Arginine"
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 residues 1 to 334 of 334 from *E.*
coli K12 : B3958"
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 phosphate reductase"

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EWQSEDIKQAAQLIAVFGCYPTASQ
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MGNSFCVESLQFYGLFTHRHQEPI
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/note="residues 1 to 256 of 258 are 84.76 pct identical to residues 1 to 256 of 258 from E. coli K12 : B3959"
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GCLVDELMKRLALPVVKNGNLRVTPADQIDIITG
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CLADGNTVTVTLLDAELGHVGKAQPGSAALVQTL
LAAGYMPIISSLIGITVEGQLMNVN
ADQAAATLAATLGAIDLILLSDVSGILDGKGQRIA
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GTRISV" |
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/note="residues 1 to 456 of 457 are 89.03 pct identical to residues 1 to 456 of 457 from E. coli K12 : B3960; residues 1 to 456 of 457 are 90.57 pct identical to residues 1 to 456 of 458 from GenPept : >gb AAL22962.1 (AE008892) argininosuccinate lyase [Salmonella typhimurium LT2]"
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/db-xref="GI:21956992"
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DSLRFDYRLAEQDIIGSVAWSKAL
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| CDS | 334453..335229 | |
| CDS | 335396..336769 | |

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 LGCAGALAGTAYAIDREQLAGWLGF
 ASAATRNSLDVSVDRDHVLELLSDAS1GMVHLSRF
 AEDLIFFNSGREAIFVLDSDRVTS
 SSLMPQQKNPDALELIRGKCGRVOGALTGMMTML
 KGLPLAYNKNDMQEDKEGLFDALDT
 WLDCLHMAALVLDGIVQVKPRCKEAAEQGYANAT
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/note="receptor for HasA and heme; residues 42 to 830 of 830 are 55.62 pct identical to residues 122 to 899 of 899 from GenPept : >emb|CAA70172.1| (Y08983) hasR [Serratia marcescens]"
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 AKVGWNEAQORLEFSYIOTQIASPNASMLSEVL
 ALSPSGKEITKIGWRNTSFTNVEN
 RNIALDYRLNPHEHISWLADATAKIYYVDTNDETDN
 ANSLFKKEYFWTQTRLKTRGLQLO
 TNTFTPSDAHQIRLKYGLEWSDKSEGYSTRKLI
 ERTTIPGPKRAITSTFAQLNYEYDD
 WLRLEGGGLRYDQFRLKGNWLHTRSFLQPYTFEN
 PCDRRRIHEQSEKPGSRCSSRPFAT
 MRWDVDRCEQQLSPTLAMGVKPGLEWLEFFGSY
 KSWRFPAMTEVLTATGTAHGSWVL
 PNPFVAAERARTWEAGFNIQOSNLIFIEDDHFAAK
 VAYFDTRIANYINLELGKAKPKFG
 GDSTFDVAYVNLLKTRFRGLEYQLSYDAGTFYT
 NINYTRM1GVNNVCSPYAWLGGLQ
 SVKYKVGKVEQJYAVENEVANNYVTCMANVLF
 GSSAYLPGDRGSLTLGSRIFDRL
 DFGTVIRYNKGYQDRSAQDENGNPLTAYVADWPK
 YIVYDLYASYKVTNNLLIRSSIEN
 ITNRAYLVNYGDTLSFAPSRRGRTIQGGFEYKF"
/gene="hasA"
*/locus-tag="y0314"**

CDS 340082..340699 /gene="hasA"
/locus-tag="y0314"
/function="transport: transport of
small molecules; cations"
/note="secreted heme-binding
protein experimentally shown to
bind heme; residues 1 to 181 of
205 are 31.60 pct identical to
residues 1 to 182 of 188 from
GenPept : >emb|CAAS7068.1|
(X81195) hasA [Serratia
marcescens]"
/codon-start=1
/transl-table=11
/product="secreted hemophore"
/protein-id="AAM83905.1"
/db-xref="GI:21956995"
/translation="MSTTIQYNSNYADYSISSSYL
REWANNFGDIDQAPAEATKDRGGSFS
GSSTILFSGTQYAIQGSSHSNPEGMIAEGDLYKYSFM
PQHTFHGQIDTLQFGKDLATNAGG
PSAGKHLEKIDITFNELDLSGEFDSGKSMTENHQ
GDMHKSVRGLMKGNPDPMLEVMA
KGINVDTAFKDLSIASQYPDSDGYMSDAPMVDTVG
VVDCHDMLAA"
gene 340850..342673 /gene="hasD"
/locus-tag="y0315"
CDS 340850..342673 /gene="hasD"
/locus-tag="y0315"
/function="transport: transport of
small molecules; cations"
/note="secretion of HasA; residues
22 to 589 of 607 are 62.14 pct
identical to residues 1 to 566 of
582 from GenPept :
>dbj|BAAL2015.1| (D83582)
metalloprotease transporter
[Serratia marcescens]"
/codon-start=1
/transl-table=11
/product="secretion ATPase, Type I
secretion system"
/protein-id="AAM83906.1"
/db-xref="GI:21956996"
/translation="MEMDAMESCKTPGASSVPPT
ILSVLAGNKKILWGIGLFTAVINL
LMLAPAIYMLQVYDRVLASANTMTLLMLTVLVLG
VFVFIGLLEWVRSAVVIRLGTQID
MQLNQPVNAAFAANLKGHNTPAAQALNDLTVLR
QFATGNALFAFFDAPWFPLYLLVI
FLLHPWLGMЛАААГАГИЛVLAWLNQWICKKPLH
DASIIITSHATQQQANANLRNADVIE
AMGMLKALRERWLMOHANFLYQQNLASDKSSRVT
AVAKSSRQALOSMMILGLGALLVIV
NEITAGVMIAGSILIGRVLGPIDQLIAVWKQWSH
ARLAYQRLSQLLAQHPSPTGMLV
PAPOGKLNVTOLMACKPGTHIPVLHSINFELQPG
DVLGLLGPGSGSKSTLAKLLVASQ
PTFSGTWRQLDSADLRSRWDKTQLGEFIGYLPQNIQ
LFRGTVAENIARFGAIDTAKVVA
AQLADVHDLILHLPQGYDTPLGDDGEGLSGGQRQ
RIALARAMYGIPRLIVLDEPDASL

DKEGEQALLASIIQLKQQGCTIVMITHKPELLSG
SDYLLFLKNGQMDLFDRTOAVLQN
IQGKDKPQAVQPEAKILNSRSRGWSNGVSYGIGPAR
TTSSPKP"
gene 342749..344077
CDS 342749..344077
/gene="hasE"
/locus-tag="y0316"
/gene="hasE"
/locus-tag="y0316"
/function="transport: transport of
small molecules; cations"
/note="secretion of HasA; residues
20 to 442 of 442 are 47.54 pct
identical to residues 17 to 443 of
443 from GenPept :
>dbj|BAA12016.1| (D83582)
metalloprotease transporter
(*Serratia marcescens*)"
/codon-start=1
/transl-table=11
/product="secretion permease, Type
I secretion system"
/protein-id="AAM83907.1"
/db-xref="GI:21956997"
/translation="MLPESVCYSVANANRQPPLQ
INSGRYLNIGGGLVVIGFIGFLWW
AGLAPLDKGVAVTGLLVAENRKVIQFLQGRIQ
QLHVTEGDEIVSGQLLVTLDDTAI
RNQRDNLQHQYLSALAAQEARNLAEQNNDLVITFP
QALLEHATQPAVERNIILQQOLLH
HRRQAHLSSEIARLSTOLTRHQARLDGLQAMRSNH
QRQSNLFQQQLDSVQLAKADGHIA
KNKLLEMESQSTSLOQARVEQSTS DIAEAKHLIDE
TEQHVLQRREQYQSENSEQLAKAQ
QNTQELVQLRNIAEYELSHTRIFAPVSGSVIALA
QHTVGGVVSSGQALMEIVFSGQPL
FVEAQLPVELIDKVAVGLPVDLNFSAFNQSNTPR
LQGSVWRIGADRIQPPFTSPYYP
LTVAILDLPTELAIIRPGMAVDVFIRTGERSLLSY
LFKFTTDLRLHALAEE"
/gene="hasB"
/locus-tag="y0317"
/gene="hasB"
/locus-tag="y0317"
/function="transport: transport of
small molecules; cations"
/note="possibly specific for
heme-HasA uptake via HasR
receptor; residues 14 to 265 of
267 are 36.90 pct identical to
residues 16 to 257 of 258 from
GenPept : >gb|AAK67308.1|
(AF283294) CjrB (*Shigella*
flexneri)"
/codon-start=1
/transl-table=11
/product="TonB-like protein"
/protein-id="AAM83908.1"
/db-xref="GI:21956998"
/translation="MNRLQOSSSDKLIFWLVGALL
ACGHIYALWWLSTASIAPIAPTSY
PAAIMMELSAEPEFMONLPONSVVGITQNIIEPA
VEQRVNQPDDIVDLPTLPEQPEGQ

REITRKEP IKVKRPAENRATS RKPVN KETQESDS
 KQSSPAAAASAMLSGT SQQVAAAV
 NSDSSHRRQQAQVS WKSRLQGHLMGF KRYPSSARK
 QQQQGTA MIRFVVVDKNGYVSSVQL
 SHSSGTSAL DREALAI IKRAQPLPKPPAELLSQG
 QITLSSLPVDFNLKRK"
gene complement (345061..3465 /locus-tag="y0318"
 24)
CDS complement (345061..3465 /locus-tag="y0318"
 24)
 /function="enzyme; oxidoreductase"
 /note="residues 1 to 486 of 487
 are 75.00 pct identical to
 residues 1 to 483 of 484 from
 GenPept : >gb|AAF95779.1|
 (AE004330) pyridine
 nucleotide-disulfide
 oxidoreductase, class I [Vibrio
 cholerae]"
 /codon-start=1
 /transl-table=11
 /product="putative pyridine
 nucleotide-disulphide
 oxidoreductase"
 /protein-id="AAM83909.1"
 /db-xref="GI:2195699"
 /translation="MKT LNVDV AVIGGGTAGLGA
 YRAAKL LTPTNV VMI EGG EY GTTCA
 RVGC MPSK LIAAAEAVH QIEKAP GFGI HPQ GK P
 LINGRE VMD RVKR ERDR FVG FV LE
 SVETI PAAD KI OGYAR FIDN NTLQ VDD H TQL TSQ
 KII AORIV IAT GS RPSW PASW NEL
 GDRL IIN DDV FNW DDLF E SVA VFG PGV GIG LE LGQ
 ALH RLGV QV KM FG VGV GAV G VGP LTD S
 IVRD YAA KT L GDEF YLDP DV KVEL M QREG DK VF I
 RYLD KSG SRP QE IMV D YV LA AT GR R
 PNV DKL GL ENTS L L DER GP QAD RL TM QT NV PH
 IFI AGD ASN QL P L L HEAS D QAR IA
 GVNAG GFPE VVPGL RRSP I S VV FS DP QI AM VG AT
 FRELA QKFSAC GC F EIGEV SF EN Q
 GRSR VML KNKG IL RI YGEO GT GR FL GA EMM GPSA
 EHI AHL LA WA H Q QOMT ID QM L DMP
 FYHPV IE EGL RT AL RD LQ SKL KLG ADE AER CL RC
 PGE"
gene complement (346619..3473 /locus-tag="y0319"
 50)
CDS complement (346619..3473 /locus-tag="y0319"
 50)
 /function="enzyme; oxidoreductase"
 /note="residues 1 to 241 of 243
 are 81.32 pct identical to
 residues 5 to 245 of 247 from
 GenPept : >gb|AAF95778.1|
 (AE004330) peroxiredoxin family
 protein/glutaredoxin [Vibrio
 cholerae]"
 /codon-start=1
 /transl-table=11
 /product="peroxiredoxin family
 protein"
 /protein-id="AAM83910.1"
 /db-xref="GI:21957000"

/translation="MFTSQEGKKVPQVTFHTRQG
 DQWIDVTTDDLFSNKTIVFSLPG
 AFTPCTSSSHLPRYNELAGVFKQHGVDSILCVSV
 NDTFVMNAWKSDQHAENITFVPDG
 NGEFTKGMMMLVEKAIDLGFGRSWRYSMVLRNGV
 VEKMFVEPNKPGDPFEVSADTML
 KYLAPDFKVQESVAVFTKPCPFCAAKQMLQDH
 GLQYEEIVLGKDATTVSRAVSGR
 STVPQIFIGGRHIGGSDDLEKYLPA"
gene 347497..348414
CDS 347497..348414
 /gene="oxyR"
 /locus-tag="y0320"
 /gene="oxyR"
 /locus-tag="y0320"
 /function="regulator; global
 regulatory functions"
 /note="residues 1 to 305 of 305
 are 86.55 pct identical to
 residues 1 to 305 of 305 from E.
 coli K12 : B3961; residues 1 to
 297 of 305 are 91.24 pct identical
 to residues 1 to 297 of 302 from
 GenPept : >gb|AAC72241.1| (U74302)
 oxidative stress transcriptional
 regulator [Pectobacterium
 carotovorum]"
 /codon-start=1
 /transl-table=11
 /product="activator, hydrogen
 peroxide-inducible genes"
 /protein-id="AAM83911.1"
 /db-xref="GI:21957001"
 /translation="MNIROLEYLVALAEFRHFR
 AADSCHVSQPTLSQIRKLEDELG
 IMLLERTSRKVLFQAGLLLVEQAKTVLREVKVL
 KEMASLQGESMSGPLHIGLILPTVG
 PYLLPQIIPMLHKTFFKLEMYLHEAQQTQNLLAQ
 DSGKLDCAILALVKETAEFIEIPL
 FDEPMNLAIYADHPWANRERVEMHELAGEKLLML
 EDGHCLRDQAMGFCFQAGADEDTH
 FRATSLETLRNMVAAGSGITLLPALAVPNERQRD
 GVCYLECYKPVPKRTIALVYRPGS
 PLRGRYEQLAEAIRDHMQERMPSLEQAI"
gene complement (348397..3497
 31)
CDS complement (348397..3497
 31)
 /gene="udhA"
 /locus-tag="y0321"
 /gene="udhA"
 /locus-tag="y0321"
 /note="residues 1 to 444 of 444
 are 84.00 pct identical to
 residues 1 to 444 of 444 from E.
 coli K12 : B3962; residues 1 to
 444 of 444 are 85.36 pct identical
 to residues 23 to 466 of 466 from
 GenPept : >gb|AAL22964.1|
 (AE008893) soluble pyridine
 nucleotide transhydrogenase
 [Salmonella typhimurium LT2]"
 /codon-start=1
 /transl-table=11
 /product="putative oxidoreductase"
 /protein-id="AAM83912.1"

| | | |
|------|--------------------------|-------------------------------------|
| | | /db-xref="GI:21957002" |
| | | /translation="MGLVKQGARVAVIERYNNVG |
| | | GGCTHWGTTPSKALRHAVSRIIEF |
| | | NQNPLYSNDNARTIKSSFAIDLNHADRVINQQTRM |
| | | RQGFYDRNHCHMFSGDASPIDANT |
| | | VNVRYADGTSDTLQADNIVIATGSRPyRPVNVD |
| | | NHERIYDSDTILQLSHEPQHVIY |
| | | GAGVIGCEYASIFRGLSVKVDLINTRDRLLAFLD |
| | | QEMSDALSYHFWNNGVVIIRHNEEF |
| | | EQIEGTTDGIVVHLKSGKKVKACCLLYANGRTGN |
| | | TSGLGLENIGLEADSRGLLKVNSM |
| | | YQTALSHVYAVGDVIGYPSLASAAYDQGRGRIAQA |
| | | MIKEANVHLIEDIPTGIYTPEI |
| | | SSVGKTEQELTAMKVPYEVGRAQFKHLARAQIVG |
| | | MDTGSLKILFHRETQKILGIHCFG |
| | | ERAAEIHIQQAIMEQKGEGNTLEYFVNNTFNPY |
| | | TMAEAYRVAALGLNRLF" |
| gene | 350003..350650 | /locus-tag="y0322" |
| CDS | 350003..350650 | /locus-tag="y0322" |
| | | /note="residues 4 to 210 of 215 |
| | | are 95.65 pct identical to |
| | | residues 19 to 225 of 234 from E. |
| | | coli K12 : B3963" |
| | | /codon-start=1 |
| | | /transl-table=11 |
| | | /product="hypothetical protein" |
| | | /protein-id="AAM83913.1" |
| | | /db-xref="GI:21957004" |
| | | /translation="MTGIMGVRAQQKERTRRSLI |
| | | EAAFSQLSAERSFASLSLREVSRE |
| | | AGIAFTSFYRFRDVDELLGTMVDESGMLRQLM |
| | | RQARQRIAKGGSVIRTSVSTFMEF |
| | | IGNNPNAAFRLLRERSGTSAFAAAREIQHFI |
| | | AELADYLLEHNMPRSFTAQEABA |
| | | MVTIVFSAGAEVLVDVIEQRQLEERLVLQLRMI |
| | | SKGAYYYWYRREOEKLAASRVE" |
| gene | 350663..351070 | /locus-tag="y0323" |
| CDS | 350663..351070 | /locus-tag="y0323" |
| | | /note="residues 3 to 115 of 135 |
| | | are 66.37 pct identical to |
| | | residues 2 to 114 of 119 from E. |
| | | coli K12 : B3964; residues 3 to |
| | | 115 of 135 are 70.79 pct identical |
| | | to residues 2 to 114 of 119 from |
| | | GenPept : >gb AAL22966.1 |
| | | (AE008893) putative inner membrane |
| | | protein [Salmonella typhimurium |
| | | LT2]" |
| | | /codon-start=1 |
| | | /transl-table=11 |
| | | /product="hypothetical protein" |
| | | /protein-id="AAM83914.1" |
| | | /db-xref="GI:21957005" |
| | | /translation="MEQSSRRETGTLLLALITGL |
| | | AINGVCAALFSALVPFSPVPLTL |
| | | ILAVALCQLQRYLNFMAPQGIPVLASACFLLGILL |
| | | YSAIVRVEYPAIGSNEFPVPAVLSVV |
| | | LVFWILFKLTRKSVQTHDADIDINNSDQPQQ" |
| gene | complement (351204..3523 | /gene="trmA" |
| | 07) | /locus-tag="y0324" |
| CDS | complement (351204..3523 | /gene="trmA" |

| | | |
|------|----------------|--|
| | | /locus-tag="y0324"
/function="enzyme; aminoacyl tRNA synthetases, tRNA modification"
/note="residues 1 to 363 of 367 are 77.41 pct identical to residues 1 to 363 of 366 from E. coli K12 : B3965; residues 1 to 363 of 367 are 77.41 pct identical to residues 1 to 363 of 366 from GenPept :>gb AAGS9169.1 AE005628-5
(AE005628) tRNA
(uracil-5)-methyltransferase
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="tRNA
(uracil-5)-methyltransferase"
/protein-id="AAM83915.1"
/db-xref="GI:21957006"
/translation="MTPNIPPIESYDHQLAEKA
RLKAMMLFQAPEPEIFRSFSPADHY
RMRAEFRVWHDDEDLYHIMFDQQTQKRIRVEQFP
VASRLINRMLDALMTAIRAEPPLL
RKLFDQIDYLSTLSGKLIASLLYHRQLDEWQK
ALELRDQLRAQQGFDLQLIGRAAKT
IMLDHDYIDEVLPVAGREMIYRQVENSFTQPNA
VNIIHMLEWALDVTOQATGDLLELY
CGNGNFSLALARFVERVLATEIAKPSVAAQYNI
AANNIDNVQIIRMSAEEFTQAMOG
VREFNRLLRGIDLGSSYNCETIFVDDPSSGLDHETV
KLVQAYPRILYISCNFETLCANLE
QLQHTHKISRALFQDFPYTHHMECGVLLKEKRH"
/gene="btuB"
/locus-tag="y0325"
/gene="btuB"
/locus-tag="y0325"
/function="membrane; outer membrane constituents"
/note="residues 31 to 653 of 653 are 64.84 pct identical to residues 2 to 614 of 614 from E. coli K12 : B3966"
/codon-start=1
/transl-table=11
/product="outer membrane receptor for transport of vitamin B12, E colicins, and bacteriophage BF23"
/protein-id="AAM83916.1"
/db-xref="GI:21957007"
/translation="MAVAYYRPWHCGIRQLSLDA
LLMIKNTMTIKKYTLTALSFTA
FSGWAQGNNTTDNNDEMVTANRFPQPKSSVLP
VDVVTRADIDRQWQSTNINDVLRL
PGVDIAQDGGMQORSSLFIRGTTNSHVLVIDGV
RLNQAGITGASDLSQIPISLVLVRI
EYIRGPRSAVYGSDAIGGVINILTGRDKPGTTL
AGLGSNGYQTYDGSTQQKLGEDTT
VTLAGNNTYSKGYDVVAGMPGAGGPRQPDRCDFM
GKMLWAGLEHQFNEQFNCFARVYG
FDNRSDYDGYTNYSNPLALIDTRKLSSRTYDTGL |
| gene | 352703..354664 | |
| CDS | 352703..354664 | |

RYKNGIYASQFIASYNRTKDYNYS
 PLFGQHHDITASLDEAEQYNLQWGNTFQLTNGMIS
 AGADWQEQRTERKSSNQNNTTADFT
 QHNTGIYLTGQQQISDVTLEGAVRSDDNSQFGWH
 STWQTSAGWEFIGYRLIGSYGTA
 YKAPNLIMOLYSAYGGNANLKPPEESKQWEGGEVGL
 TGPLTWRLSAYRNNDIDQLIDYSNL
 TNGYFNINAKATIKGVVEWTGSFDTGPLSHQVTLEY
 LDPRNAUTHEILVRRAKQQVKYOL
 DWQVADLDWSVTYQYLGQRYDKDYSTYPEETVEL
 GGVSLWDLAVSYPVTSHLTVRGRI
 ANLFDKDKEYMVYVGQTPGREYYFTGSYNF"

 gene 354573..355472
 CDS 354573..355472

 /gene="muri"
 /locus-tag="y0326"
 /gene="muri"
 /locus-tag="y0326"
 /function="enzyme; murein
 sacculus, peptidoglycan"
 /note="required for biosynthesis
 of D-glutamate and peptidoglycan;
 residues 9 to 299 of 299 are 71.13
 pct identical to residues 1 to 287
 of 289 from E. coli K12 : B3967;
 residues 13 to 299 of 299 are
 73.17 pct identical to residues 1
 to 283 of 283 from GenPept :
 >gbl|AAL22969.1| (AE008893)
 glutamate racemase [Salmonella
 typhimurium LT2]"
 /codon-start=1
 /transl-table=11
 /product="glutamate racemase"
 /protein-id="AAM83917.1"
 /db-xref="GI:21957008"
 /translation="MPTCLIKIMRWFMATKQPDA
 NTTSREAITSKADSPPRPTALIFD
 SGVGGLSVYEQIRQLLPDLHYIYAFDNVAFFYGE
 KSGHEFIVERVLEIVTAVQQRHPLA
 IIVVIACNTASTVSLSPALRERFAPFVVGVVPAIKP
 AVRLLTRNGVVGLLATRATVHASYT
 LLDLIARFATDCIKIELLGGSELVEVAETKLHGGVV
 PLEVLLKKILHWLMSRREPPTDTIVL
 GCTHFPLLTEELAQVLPPEGTRMVDSGAAIARRTA
 WLISSQENVISSQDENIAYCMA LD
 EDTDALLPVLQSYGFFKLQKLPI"

 gene 355930..357514
 rRNA 355930..357514

 /locus-tag="yr005"
 /locus-tag="yr005"
 /product="16S ribosomal RNA"

 gene 357608..357680
 tRNA 357608..357680

 /locus-tag="yt003"
 /locus-tag="yt003"
 /product="tRNA-Glu"
 /note="anticodon: TTC"

 gene 357936..360842
 rRNA 357936..360842

 /locus-tag="yr006"
 /locus-tag="yr006"
 /product="23S ribosomal RNA"

 gene complement(360878..3612
 CDS 70)

 /locus-tag="y0327"

 complement(360878..3612 /locus-tag="y0327"
 70)

 /note="residues 5 to 36 of 130 are
 50.00 pct identical to residues 11
 to 48 of 50 from GenPept :

>emb|CAB67146.1| (AJ271079)
 hypothetical protein [Oenothera
 elata subsp. hookeri]
 /codon-start=1
 /transl-table=11
 /product="hypothetical"
 /protein-id="AAM83918.1"
 /db-xref="GI:21957009"
 /translation="MAERTGLEPATPCVTGRYSN
 QLNRYSTDSFTCIFFLYPIRASA
 LRCAKPILLAITVTRCHSDNSCLMPGSVLLSHGE
 TPHYHRYGVSSLSSAWDQVGPF
 YGRQANSVLINPOTSNTCQFVNNTISERR"
 gene 360950..361069
 rRNA 360950..361069
 gene 361193..361272
 tRNA 361193..361272
 gene 361278..361350
 tRNA 361278..361350
 gene 362330..363286
 CDS 362330..363286
 gene 363372..364862
 CDS 363372..364862

/locus-tag="yr007"
 /locus-tag="yr007"
 /product="5S ribosomal RNA"
 /locus-tag="yt004"
 /locus-tag="yt004"
 /product="tRNA-Asp"
 /note="anticodon: GTC"
 /locus-tag="yt005"
 /locus-tag="yt005"
 /product="tRNA-Trp"
 /note="anticodon: CCA"
 /locus-tag="y0328"
 /locus-tag="y0328"
 /function="putative regulator"
 /note="residues 1 to 318 of 318
 are 75.78 pct identical to
 residues 1 to 318 of 318 from E.
 coli K12 : B4227"
 /codon-start=1
 /transl-table=11
 /product="solute-binding
 periplasmic protein of ABC
 transporter"
 /protein-id="AAM83919.1"
 /db-xref="GI:21957011"
 /translation="MYRRLLLAAAVTAAMCSAVQ
 AAPLVVGFSQIGSESGWRSAAETKV
 AKQEAEKRGITLKIAADAQQKQENOIKAVRSFIQAQ
 GVDAIFIAFPVATGWPVPLQEAKE
 AKIPVFLLDRMIEVNPDPSLYTAAVASDSVYEGKV
 AGEWLLQDVAGKPCNVELQGTVG
 SSVAIRRKGFADGIAASAPGVKIIIRSQSDFTRS
 KGKEVMESEFIKAEQNGKNICAVYA
 HNDDMAIGAIQAIKEAGLKPGSDIKIVSIDGVPD
 IFKAMSSGEANATVELTPNMAGPA
 LDLALVLKKDGTOPPKFIQTESRLLQPDATKQEY
 ELKKSLGV"
 /locus-tag="y0329"
 /locus-tag="y0329"
 /function="putative transport"
 /note="residues 4 to 376 of 496
 are 62.73 pct identical to
 residues 9 to 381 of 417 from E.
 coli K12 : B4228; residues 4 to
 494 of 496 are 67.20 pct identical
 to residues 9 to 499 of 500 from
 GenPept :
 >gb|AAG59426.1|AE005655-5
 (AE005655) putative ATP-binding

| | | |
|------|----------------|--|
| | | component of ABC transporter
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="putative ATP-binding
component of ATP transport system"
/protein-id="AAM83920.1"
/db-xref="GI:21957012"
/translation="MEILLEVRGLSVEFFPGVKAL
DSVDFSLQRGEVVALLGENGAGKS
TLIKALTGVYKRSAGEVLLDGKAVCPIDTADAQL
MGIGTVYQEVNLLPNISVAANLFI
GREPLRWGLIDHNMNQQAALKLTGYGLTLDVQQ
PLANFSIAIQQIVAIARAVDLSAK
VLILDEPTASLDAKEVSMLLDILCQLRDQGIGMV
FVTHTFLDQVYRISDRITVLRNGKL
VGTKTVAELPRIELVOMMLGHSHFDEQLLKRGHEHS
ITNKNPVLVEFKNYGRGGVVENFDL
SVSPGEIVGLAGLLGLSGRRTETAQLIIFGITTPTDG
EAKIQGKPVKIRTPRKASKEFGFYG
CPEDRKTEGIVGAATVRENIILALQAZQRGLRPL
SMREQTQIAADDIPIQQLGIRTPSPE
QQIQYLSGGNNQKVLLARWLATKPRFLIILDEPTR
GIDVGAHAEIIRLIEKLCEGLAL
LIISSELEELAGYADRIIVLDRDRRHVAQLDHDEI
SVPAIMQAIAVQ"
/locus-tag="y0330"
/locus-tag="y0330"
/function="putative transport"
/note="residues 4 to 326 of 339
are 70.67 pct identical to
residues 4 to 325 of 341 from E.
coli K12 : B4230; residues 4 to
326 of 339 are 70.37 pct identical
to residues 4 to 325 of 341 from
GenPept :
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(AE005655) putative transport
system permease protein
[Escherichia coli O157:H7 EDL933]"
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system inner membrane permease
protein"
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/db-xref="GI:21957013"
/translation="MGNRSLSLMTQRPRKVKWVLP
KGATOFGALAVILLIDSIVAPAHFF
SIHQDGRLFGSIIDILNRGAPVALLAGMHLVI
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SAGYFMTVTLALSIVAGLCGLWNGFLVAVLQIQ
PIVATLMLMVAGRGAQQLITEGOI
VTFDGGGLATLGSSITLMLYLPMSVVIACSMILVW
LLTRKTALGLFIESVGINLRSARN
AGVSTRVLIAVVVICGVCAAVAGIIVTADIRGA
DANNAGLWLELDAILAVLVIGASL
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LVLKAIIVVLAFLVQSPMISLSHL FQRK"
/locus-tag="y0331"
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/function="putative transport" |
| gene | 364874..365893 | |
| CDS | 364874..365893 | |
| gene | 365893..366885 | |
| CDS | 365893..366885 | |

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/note="residues 9 to 330 of 330
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residues 1 to 318 of 323 from E.
coli K12 : B4231"
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permease protein"
/protein-id="AAM83922.1"
/db-xref="GI:21957014"
/translation="MLKRNVPPLLITIAVFILGYA
FCLSQFPSSSRVWC DLLTDNAF
LGIVAVG MFTVILSGGIDL SVGSVIAFTGVLLAK
LIGTYG IHPVYAF AIVLVMGAMFG
ALMGW IIDS LKLPFAI ITLAGMF FIRGMSFIVSE
ESLPINHPI YETLANYA WRPVPGGG
RFTLLA FIMLMVVA F GILLAH HTRFGHN VYA IGG
NSVSAGLMGPV VRRTT I KIYMLSS
T LAALSGIVFSL YTSAGY ALAAS GVEL DAI AAVV
IGGTLLAGGI GTVFGT LFGVLIQG
LIQS YITFDGT LSSW T KIVIGILL FSFIVI QKA
MSAFYLNRRSRPQSSPLTPV"
gene complement(366872..3677 /locus-tag="y0332"
53)
CDS complement(366872..3677 /locus-tag="y0332"
53)
/note="residues 84 to 280 of 293
are 50.99 pct identical to
residues 3 to 190 of 198 from E.
coli K12 : B3762; residues 1 to
281 of 293 are 62.32 pct identical
to residues 1 to 272 of 278 from
GenPept : >emb|CAD09467.1|
(AL627279) possible LysR-family
transcriptional regulatory protein
[Salmonella enterica subsp.
enterica serovar Typhi]"
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/protein-id="AAM83923.1"
/db-xref="GI:21957015"
/translation="MDTELLKTFLEVS RTRHFG R
AAESLYLTQSAVSFRIRQLENQLG
ANLFTRHRN NIRLTPAGERL VPYAEMLLNTWRLA
KKEVIHSLSQH TELSIGATASLWEA
YLTPWLQOLYEQQEELRLEARIALRNSLVLKQLHE
RQLDL LITTEPFKMDELA CLLLGH
FSLRLYSSFSL DLPKEDDT PNEHKNASE VPYIKL
EWGADFHQ QENRLLDSEQAPILT
TSAHLTRQ LLETTGGCAFLPEH WQKEYPQLV IHP
DIPPIVRPL YAVWLQNSDQ QALIR
QLLKT PMNNATOSVTRE"
/locus-tag="y0333"
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/note="residues 29 to 140 of 140
are 83.03 pct identical to
residues 1 to 112 of 112 from E.
coli K12 : B3764"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
gene 367788..368210
CDS 367788..368210

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EPVTEEEQRFVAVCRGEREPPVSAE
EKVWSKYVIRTRQPKRFHTLSGGKPQMDAVEDYT
DSDD"
gene complement(368467..3700 /locus-tag="y0334"
11)
complement(368467..3700 /locus-tag="y0334"
11)
/function="putative regulator"
/note="residues 1 to 513 of 514
are 62.76 pct identical to
residues 4 to 515 of 516 from E.
coli K12 : B3765"
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regulator"
/protein-id="AAM83925.1"
/db-xref="GI:21957017"
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IPADKLAHYEFGLELALSGALRRVSGAIPAAALTC
SEANRQLILPTANGLEIGLIPQGN
SWADHLLAVCGFLQGENFLAQQPFEPPAPSPDN
HLDLHDIIIGQSQAKRALEIAAAAGG
HNLLLGPPGTGKTMLATRLTGLLPPPLTDQEALE
AAAITGLLHSNALPTQWRCRRAFRA
PHHSASMAALIGGGSIPRPGEISLAHNGVLFLD
LPEFERRVLDSLREPLESCEIIIS
RAAAKICCPAKVQLIAAMNPSPSGHYGVHNRTP
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VPLLPGMLGAQKNQGESSATVKQORVLQARQRQM
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/locus-tag="y0335"
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/locus-tag="y0335"
/function="leader; amino acid
biosynthesis: Isoleucine, Valine"
/note="residues 1 to 32 of 32 are
81.25 pct identical to residues 1
to 32 of 32 from E. coli K12 :
B3766"
/codon-start=1
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/product="ilvGEDA operon leader
peptide"
/protein-id="AAM83926.1"
/db-xref="GI:21957018"
/translation="MKAILQVINLVLISVVVIII
PPCGAALGRRKA"
/gene="ilvG"
/locus-tag="y0336"
/gene="ilvG"
gene 370374..370472
CDS 370374..370472
/gene="ilvL"
/locus-tag="y0335"
/gene="ilvL"
/locus-tag="y0335"
/function="leader; amino acid
biosynthesis: Isoleucine, Valine"
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81.25 pct identical to residues 1
to 32 of 32 from E. coli K12 :
B3766"
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peptide"
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/db-xref="GI:21957018"
/translation="MKAILQVINLVLISVVVIII
PPCGAALGRRKA"
/gene="ilvG"
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/gene="ilvG"
gene 370613..372259
CDS 370613..372259

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/locus-tag="y0336"
/function="enzyme; amino acid
biosynthesis"
/note="residues 1 to 548 of 548
are 79.92 pct identical to
residues 1 to 548 of 548 from
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>gb|AAG58963.1|AE005608-4
(AE005608) acetohydroxy acid
synthase II [Escherichia coli
O157:H7 EDL933]*
/codon-start=1
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/product="acetohydroxy acid
synthase II"
/protein-id="AAM83927.1"
/db-xref="GI:21957019"
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LIGTDAFQEIDVVLGLSLACTKHSFLVESLDALPE
IMAEAFIAIASGRGPGLDIPKD
IQLAVGELTPHLKPVEEHSVDSAELQHAWDMA
NAQKPMLYVGGGVGMAQAVPALRD
FIAMTIGIPAVATLKGGLGAPDIAHPCYLGMIGMHG
TKAANFAVQDCDLLVAVGARFDDR
VTGKLNTFASKAKVIIHMDIDPAELGKLQRQHVHAL
QGNLNVLLPALQQPLNIQSWRDEV
MALKQQHHWRYDHPGQAIYAPLLLKKQISERCAPE
TVVTTDVQHQMWTAQHMNFTRE
NFITSSGLTGMGFVPAAVGAQMARPDMMVICVS
GDGSFMMNVQELGTIKRKQLPLKI
VLLDNQRLGMVRQWQOLFFDGRYSETNLSNDNPDF
ITLASAFDIPGQRITRKDQVDAAL
DALFNSEGPYLLQVSIIDELENVWPLVPPGAGNET
MLEKIS"
gene          372461..373462
/CDS           372461..373462
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/locus-tag="y0337"
/gene="ilvE"
/locus-tag="y0337"
/function="enzyme; amino acid
biosynthesis: Isoleucine, Valine"
/note="residues 27 to 332 of 333
are 91.17 pct identical to
residues 3 to 308 of 309 from E.
coli K12 : B3770; residues 27 to
332 of 333 are 91.50 pct identical
to residues 3 to 308 of 309 from
GenPept :
>gb|AAG58965.1|AE005608-6
(AE005608) branched-chain
amino-acid aminotransferase
[Escherichia coli O157:H7 EDL933]*
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/product="branched-chain
amino-acid aminotransferase"
/protein-id="AAM83928.1"
/db-xref="GI:21957021"
/translation="MSPVSRSYNLIHYRYAPDAP
EGKKRTKKADYIWFNGEMVPWAE

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 EQGIDAMSSWNRVAPNTIPTAAKAGNNYLSSLL
 VGSEARRHGYQREGIALDVHGYLSE
 GAGENLFEVKDGILFTPPTSSALPGITRDAIIK
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gene 373725..375623
CDS 373725..375623
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 /function="enzyme; amino acid biosynthesis: Isoleucine, Valine"
 /note="residues 37 to 632 of 632 are 86.04 pct identical to residues 4 to 605 of 605 from E. coli K12 : B3771"
 /codon-start=1
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 /db-xref="GI:21957022"
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 HGGMLYSLPSRELIAADSVEYMVNAHCADAMVCIS
 NCDKITPPGMLMASLRLNIPVIFVS
 GGPMEAGTKLSDKIIKLLDIDAMIQGANPNVSD
 EESAQIERSACPTCGSCSGMFTAN
 SMNCLNEALGLALPGNGSLLATHADRQLFLDAQ
 KHIVALTCKRYYEQDDVSAALPRNIA
 NKAAPENAMILDIAMGGSTNTVLHLLAAQEGEI
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 LGLNLQTLEAYDVMLTQDEGVVKQ
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 TREHAYSQDGLAVLYGNIAADGC
 IVKTAGVDKDSLTFRGPAAKVFESQDEAVEAILGG
 KVVAGDVVVIRYEGPKGGPGQMEM
 LYPTTYLKSMGLGKSCALLTDGRFSGGTGSLSIG
 HVSPEAASGGLIGLVLQDGFINID
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gene 375629..377173
CDS 375629..377173
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 /locus-tag="y0339"
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 /locus-tag="y0339"
 /function="enzyme; amino acid biosynthesis: Isoleucine, Valine"
 /note="residues 1 to 514 of 514 are 84.63 pct identical to residues 1 to 514 of 514 from E. coli K12 : B3772; residues 1 to 514 of 514 are 85.01 pct identical to residues 1 to 514 of 514 from GenPept : >dbj|BAB38129.1| (AP002566) threonine deaminase

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[Escherichia coli 0157:H7]
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(dehydratase)"
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/db-xref="GI:21957023"
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ACGVVTASAGNHAQGVALSAHKMG
IKALIVMPVATADIKVDAVRAFGGEVLLFGANFD
EAKTKAIALAOEGYTFVPPFDHP
AVIAQGGTLAMELLQQDAHLDRVFVPGGGGLVA
GVAVLIKQLMPQIKVIGVEAEDP
CLRALDAGQPVDLARVGLFAEGVAVKRIGDEPF
RLCQEYLLDDVITVDSDAICAAVKD
LFEDVRAIAEPSGALALAGLKKYVQQHNIQGERL
AHVLSGANVNPFHGLRYVSERCLEG
EQREALLAUTPIEQKGSSFLRFCELLGGRSUTEFN
YRYADAENACIFVGVRLTGYAER
VEILAEQLDKGYQVDSLSDDEMAKLHVRYMVGR
PSKPRLRERLFSFEFFESPAGALLKF
LHTLGTTHWNISLFHYRSHTDFGRVLAAFELSAT
EPQFEERLAALGYCHDETDPNP KFFLAG"

gene complement(377304..3777 /locus-tag="y0340"
89)
CDS complement(377304..3777 /locus-tag="y0340"
89)
/note="residues 7 to 161 of 161
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residues 6 to 167 of 176 from
GenPept : >emb|CAD02952.1|
(AL627277) putative exported
protein [Salmonella enterica
subsp. enterica serovar Typhi]"
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/protein-id="AAM83931.1"
/db-xref="GI:21957024"
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YSIPKPSADGFYTIIWFWDGDGYK
EEGKYDRLCFSDMNNTKNCIEKEKYMTIYKIKND
EPLFSFDGNRYFLNENNKKIVKMKR E"
gene complement(377848..3783 /locus-tag="y0341"
30)
CDS complement(377848..3783 /locus-tag="y0341"
30)
/note="residues 7 to 153 of 160
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residues 6 to 152 of 176 from
GenPept : >emb|CAD02952.1|
(AL627277) putative exported
protein [Salmonella enterica
subsp. enterica serovar Typhi]"
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/protein-id="AAM83932.1"

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EEGKYDERRCFEDMKTSKNCIDKNSLMIIRNSQYN
VMSFTLDGSIYQLKNGEIVKMKRE "
gene complement (378389..3788 /locus-tag="y0342"
50)
CDS complement (378389..3788 /locus-tag="y0342"
50)
/note="residues 5 to 146 of 153
are 39.35 pct identical to
residues 8 to 152 of 176 from
GenPept : >emb|CAD02952.1|
(AL627277) putative exported
protein [Salmonella enterica
subsp. enterica serovar Typhi]"
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/db-xref="GI:21957026"
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RCFEDMKTSKNCIDKNSLMIIRNSQYNVMSFTLD
SGIYQLKNGEIVKMKHE"
gene complement (378834..3797 /locus-tag="y0343"
89)
/note="disrupted by frameshift"
/pseudo
gene complement (380665..3815 /gene="ilvY"
49)
/locus-tag="y0344"
CDS complement (380665..3815 /gene="ilvY"
49)
/locus-tag="y0344"
/function="regulator; amino acid
biosynthesis: Isoleucine, Valine"
/note="residues 2 to 294 of 294
are 73.72 pct identical to
residues 1 to 293 of 297 from E.
coli K12 : B3773; residues 2 to
294 of 294 are 74.06 pct identical
to residues 1 to 293 of 297 from
GenPept :
>gb|AAG58968.1|AE005608-9
(AE005608) positive regulator for
ilvC [Escherichia coli O157:H7
EDL933]"
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ilvC"
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/db-xref="GI:21957027"
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AYSHLPPILDRFRARHPLVEIKLTGDAADAVNK
VQSNEADLGIAGRPEVLPTSVAFT
QIGEIPLVLIAPALPCAVRSQVAEKPDWAMIPF
ILPEHGPSRKRIDLWFRQRITNP
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/locus-tag="y0345"
/function="enzyme; amino acid
biosynthesis: Isoleucine, Valine"
/note="residues 1 to 492 of 492
are 92.07 pct identical to
residues 1 to 491 of 491 from E.
coli K12 : B3774; residues 1 to
492 of 492 are 92.27 pct identical
to residues 1 to 491 of 491 from
GenPept : >emb|CAD09408.1|
(AL627279) ketol-acid
reductoisomerase [Salmonella
enterica subsp. enterica serovar
Typhi]"
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reductoisomerase"
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VNLTDPDKOHSAAVVKAVQPLMKEGAALGYSHGFNI
VEVGEQVRKDITVVMVAPKCPEGTE
VREEKRGFVGPTLIAVHPENDPKGEGMAIAKAW
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MGEQTILLCGMLQAGSLLCFDKLVESEGTDAAAYAEK
LIQFGWETITEALKQGGITLMMDR
LSNPAFKLRAYALSEQLKEIMAPLFQKHMDDIISG
AFSSGMADWANDDVKLINWREET
GRTAFENAPQFEGKISEQEYFDHGVLMIAMVKAG
VELAFETMVDGSIIEESAYYESLH
ELPLIANTIKRRLYEMNVNVIQDTAEYGNYLFA
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MKRIAVAG"
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/note="residues 15 to 60 of 66 are
34.78 pct identical to residues
525 to 567 of 612 from GenPept :
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Phospholipase like protein
[Arabidopsis thaliana]"
/codon-start=1
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/protein-id="AAM83936.1"
/db-xref="GI:21957030"
/translation="MLYYEPEFLGSLRQEAYNTY

gene 383887..385329
CDS 383887..385329

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/locus-tag="y0347"
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/note="residues 340 to 454 of 480
are 44.16 pct identical to
residues 257 to 376 of 386 from
GenPept : >emb|CAD16923.1|
(AL646075) probable transmembrane
protein [Ralstonia solanacearum]"
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/protein-id="AAM83937.1"
/db-xref="GI:21957031"
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IATISAGSVAAMIALGIVYOTKVG
ESSERPPGWNVSPKFVGSISSLAMGLPATESLAS
QGENMALPVRMRIIDAKDWIGCTEI
YAVKTGVAGVLPKVKVGAQYDESTGVYTTDS
TPPRTLIFTPAOPPGAEATRPLAP
PGSTPATLQHTGEMIIKFVITPTILPLPQLYARD
FHDIYIWFADSGLEPVVYVLNSP
YGKTTAKGKYSGRDFNPDKAGGIKNLDWKEIKI
RGEGVDEVKLHTRRFGELEDNKLML
IERLEKILTNLKTATDIDKRFYTHEIRELERYRM
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gene complement (386990..3878
08)
CDS complement (386990..3878
08)

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/function="putative factor;
folding and ushering proteins:
Chaperones"
/note="pili assembly; residues 42
to 262 of 272 are 46.46 pct
identical to residues 7 to 227 of
237 from GenPept :
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(AE004640) probable pili assembly
chaperone [Pseudomonas
aeruginosa]"
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/transl-table=11
/product="putative pilus
chaperone, PapD family"
/protein-id="AAM83938.1"
/db-xref="GI:21957032"
/translation="MHMRKWLSVSNNIMLSRINR
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LIMSALATASAVASVIAERTRIVSEGSTEESQL
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ADRESAFWLNIYEIPFKATPKSGD
ESFVTLALRMQYKVFYRPKNLPAFPGDILGKALTF
SLERNNGDSALIKVNNTPTYYASFA
ALTIGSAEGPPEMVAPFSQLDFPLNRAPISDNKT

VNFDLIDDLGNRNSFSHELK"
gene complement (387774..3889 /locus-tag="y0349"
46)
CDS complement (387774..3889 /locus-tag="y0349"
46)
/note="residues 2 to 390 of 390
are 45.88 pct identical to
residues 56 to 453 of 453 from
GenPept :
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(AE004640) hypothetical protein
[Pseudomonas aeruginosa]"
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/transl-table=11
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/translation="MGSRDDNNNGSLNLP SIVDLS
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IRFTNLATGEYAAWIKGRRLTGLDTDSSGRILV
KAKNFSNVYTELFRIDYARS GANN
TPS YLYGRS QPNAYIAFKGPGITGPIEGTD SYSN
WPGWISTWPASLGLYKYVTFRRIT
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VGIRIYRNNSPMYLLSKNV TQ TGN
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ISGQTVTAGAVNAHAQV VIRVQ"
gene complement (389158..3917 /gene="fimD"
85)
/locus-tag="y0350"
CDS complement (389158..3917 /gene="fimD"
85)
/locus-tag="y0350"
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envelope: outer membrane
constituents"
/note="fimbrial biogenesis;
residues 31 to 874 of 875 are
46.38 pct identical to residues 25
to 860 of 872 from GenPept :
>gb|AA05518.1|AE004640-7
(AE004640) probable fimbrial
biogenesis usher protein
[Pseudomonas aeruginosa]"
/codon-start=1
/transl-table=11
/product="outer membrane usher
protein FIMD precursor"
/protein-id="AAM83940.1"
/db-xref="GI:21957034"
/translation="MVQARVILKKNFSGRRKALT
LCITLILHIDTAFGQEEPKNFED
ESLF LGTKYASGLTQLNKNS ITAGNYDAVDVLV
NNKLFKRM SVQFIKDANSSEVYPC
LSDELLTAA GVELGREN STPPKEPHVTEANTPIT
ETHAPTNQCLPLSTRVKGASFRFD
QAKLRLELSIPQALLQKRPRGYIERAEWQE GEKL

AFINYSANAYRSSTRGQQKRTSDF
 GFIGLKSGINLGLWQVRQOSNVRYASNDGSDTQ
 WNSIRTYVQRPIPQLDSQLTLGET
 FTDSLTLFGSMSFLGAKMATTQDRMWPSMRGFSPE
 VRGVASTNARVIIRQNREIYETN
 VAPGPFFVINDLFSTSSQGDLNVEVIEANGSRSTF
 TVPFSAVPDMSMRGVSYNAVIGE
 SRDFTNIIDNYTFDFTYERGLTNQLTANSGVRLAK
 DYTALLAGGVLGTPVGALGLNATY
 SHAKVENDKTQDGWRM0QATYSQTFNQTTGTTFSLA
 GYRYSTKGYRDNDVFGVRSMQKN
 GGTWDSTSYYKQRSQFTTINQDGLGNWGQLYASAS
 TSDYNNDTARDTQOLQLGYSNSYQQ
 ISYNLAVSRQRSSVYTSTLYNWDS PDTDETATTTR
 YGNTENIAFTVSIPLNIGSNNQY
 LSMASARNPKSGNNYQTSLSGTAGERNSFNYALN
 AGYDDSNFGSSSNNWGANVQKQFP
 NATVNGSYSRGNNYTYQYGAGARGAAVIHRQGVTL
 GPYLGETFGLIEANGA0QGARIDSN
 GFALVPALTPTVNYNTIGLDTKGINRNTELKENQG
 RRVFYAGAAVKVKFETLTGYAVLI
 QAEEGEGLPLGADVYNNSKDELVMVGQGNQIYARI
 ADNKGTLDVRGESSGDQCOLPYA
 FNRQDTEQDIHITASCR" " "
gene complement (391813..3925 / locus-tag="y0351"
CDS 68)
 complement (391813..3925 / locus-tag="y0351"
 68)
 /function="putative factor;
 folding and ushering proteins;
 Chaperones"
 /note="pilus assembly; residues 24
 to 242 of 251 are 43.69 pct
 identical to residues 16 to 237 of
 248 from GenPept :
 >gb|AAG05517.1|AE004640-6
 (AE004640) probable pili assembly
 chaperone [Pseudomonas
 aeruginosa]"
 /codon-start=1
 /transl-table=11
 /product="chaperone"
 /protein-id="AAM83941.1"
 /db-xref="GI:21957035"
 /translation="MTSEGTLLMLSITYARHYHLY
 FVTLLVAMSLSFANASVVMTGRI
 IYPAAASEHSIQLTNNDNFPNAVQVWLDSGDEKS
 TPEIGKAFIVTPTPFRIEANSQ
 TLRLKYTGSGLTDRESVYFLNLQIPPVNKVEK
 DNKMLVLLRNRIKVYFPRPESIIGR
 VDQVSTALTFSLRKGQTNLVLTGKNPFTGFYATIA
 SGEIVSGSIKLKVKSNSMIAPMSQV
 EWVIPNASVSSSATINFLIMNDFGGGDAGSYRI"
gene complement (392608..3931 / locus-tag="y0352"
CDS 38)
 complement (392608..3931 / locus-tag="y0352"
 38)
 /function="structural component;
 cell exterior constituents;
 surface structures"
 /note="fimbrial biogenesis;
 residues 1 to 175 of 176 are 49.15

pct identical to residues 3 to 177
 of 178 from GenPept :
 >gb|AAL19294.1| (AE008710)
 putative fimbriae; major subunit
 [Salmonella typhimurium LT2]
 /codon-start=1
 /transl-table=11
 /product="fimbrial protein
 (precursor)"
 /protein-id="AAM83942.1"
 /db-xref="GI:21957036"
 /translation="MKKITLAIALFSASTTVAMS
 ASNNTITFQGEVTAQTCSTVNGL
 EANPVVLLPTVSSSDLASGQTKGKTTFTLGVSG
 CTSGSDDLIKTIVFIGSLVTATGN
 LQNTGTAGNVELQLLKDTATTGIDLNGLAQDG
 IVLLLAGDTSAAHDFAVQQYYATGQS
 TPGSVIAVASVQYAVSYL"

repeat-region complement(393913..3952 /note="insertion element"
 27)
 /insertion-seq="IS285"

gene complement(393948..3951 /locus-tag="y0353"
 56)

CDS complement(393948..3951 /locus-tag="y0353"
 56)
 /function="IS and transposon
 related functions"
 /note="residues 1 to 402 of 402
 are 100.00 pct identical to
 residues 1 to 402 of 402 from
 GenPept : >gb|AAC13227.1|
 (AF053947) transposase [Yersinia
 pestis]"
 /codon-start=1
 /transl-table=11
 /product="putative transposase"
 /protein-id="AAM83943.1"
 /db-xref="GI:21957038"
 /translation="MDEKKLKLAKAAELAKGLKTE
 ADLNAFSRMLTKLTVETALNAELT
 EHLGHEKNTPKSGSNTRNGSSKTLCLCDGEIEL
 NTPRDRENTEFQPLIKNQNTRITQ
 MDSQILSLYAKGMTREIVATFKEEMYDADVSPTL
 ISKVTDVAKEQVAEWNQRQLDALY
 PIVYMDC1IVKVRQNGSVINKAVFLALGINTEGQ
 KELLGMWLAENESEGAKFWLSVLTTEL
 KNRLGLQDILIAACVDGLKGFPDAINSVYPQTHIQL
 CIIHMVRNSLKYVSWKDYKAVTSG
 LKMYVQAPTEEAALMALDKFAEAWDDKPQISKS
 WRTHWENLNTFGGYPPDIRKAIYT
 TNAIESVNVNSVIRAAIKRKVFPTDDSVRKVVYLA
 IKDASKWMSMPIQNWRRLAMSRII
 EFGDRLSDHL"

gene complement(395253..3960 /locus-tag="y0354"
 44)

CDS complement(395253..3960 /locus-tag="y0354"
 44)
 /function="enzyme; global
 regulatory functions"
 /note="residues 8 to 258 of 263
 are 39.45 pct identical to
 residues 3 to 256 of 288 from"

GenPept : >gb|AAC27745.1|
(AF061240) glutamine
cyclotransferase precursor [Carica
papaya]"
/codon-start=1
/transl-table=11
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cyclotransferase"
/protein-id="AAM83944.1"
/db-xref="GI:21957039"
/translation="MEILNIPRRCFTFLIIITY
SFPLSFADSKPLKYTFEVIRKIPH
DETSFTQGLVIDDGKLYETTGLYKNSKIRELDLT
NGKVIRSVNLDPDNIFGEGITKLGD
SFYVLTWKEKKAAFVINPNDLKIIKTFNYEGEGWG
LTTDGINLIMGDGSCTLYFRNPAD
FSIIKKISVTDFGRRIEKINELEWIDGMIYANVW
YSDAILVIEPENGRRVVKWIELSGL
QFMLDSVNRNTLNGIAYDKSKNKIYLTKGNWS
NIFEVKELTSK"
gene complement (396283..3965 /gene="ppiC"
79)
/locus-tag="y0355"
CDS complement (396283..3965 /gene="ppiC"
79)
/locus-tag="y0355"
/function="enzyme; proteins -
transliteration and modification"
/note="rotamase C; residues 6 to
98 of 98 are 67.74 pct identical
to residues 1 to 93 of 93 from E.
coli K12 : B3775"
/codon-start=1
/transl-table=11
/product="peptidyl-prolyl
cis-trans isomerase C"
/protein-id="AAM83945.1"
/db-xref="GI:21957040"
/translation="MVTVMANKASALHILVDDE
KQANDILAQLNNGANFQELAKKFS
NCPSKRNGGDLGFEFNKGDMVPAFDKAVFSCCELLQ
PYGFVKTQFGYHIKVLYRS"
gene 396714..398789 /gene="rep"
/locus-tag="y0356"
CDS 396714..398789 /gene="rep"
/locus-tag="y0356"
/function="enzyme; DNA -
replication, repair,
restriction/modification"
/note="residues 19 to 686 of 691
are 85.02 pct identical to
residues 1 to 668 of 673 from E.
coli K12 : B3778; residues 19 to
686 of 691 are 85.32 pct identical
to residues 1 to 668 of 673 from
GenPept :
>gb|AAG58972.1|AE005609-4
(AE005609) rep helicase, a
single-stranded DNA dependent
ATPase [Escherichia coli O157:H7
EDL933]"
/codon-start=1

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/transl-table=11
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single-stranded DNA dependent
ATPase"
/protein-id="AAM83946.1"
/db-xref="GI:21957041"
/translation="MAFWYNSLPRKPIEQQPSVRL
LNPSQEEAVEFVTGFCVLVLAGAGS
GKTRVITNKIAHLIRCGYQPKHIAAVTFTNKA
REMKERVAOTLGRKEARGLMIAATF
HTLGLEIILKEYVALGMKSNSFLFDAQDMGLLK
DLTHKWLLEDKTLQQLVSAISNW
KNDLDDPAAAATARSERDKLFVHCYGLYDAHLK
ACNVLDFFDLISLPTLLLQKNLEV
RERWQNRLLRYYLVEYQDINTSQYQMVKLLVGNR
ARFTVVGDDDSQIYSWRGARPQNL
VLLNEEDFALRVIKLEQNYRSSGRILKAANILIA
NNPHVFEKKLFSELSYGDELKVIT
ANNEDHEAERVVGEELIAHHFVKKTQYSDFAILYR
GNHQSRLEFKLMMQNRIPYRISGG
DSFFSRPEIKDLLAYLRLVLTNQDDDSAFLRIVNT
PKREIGAAVTQKLGEWEANLRNKS
FRASFDLGLGEHLKGRRGLESLQRFTHWMDGIIRL
VEREPVAAVRDLIHGIDYESWLF
TAPSPKAEMMRMKVNVLIFSWMTLEMLEGSELDEP
MILIQVTVRTFLRDMMERGESDEE
LDQVQLMLTHASKGLEFPYVFLVGMEEGLLPHQS
SIDEDNVDEERRLAYVGITRAQRE
LFFTLCKERRQYGELEIRPEPSRFLMELPQDDLNW
ENERKAVSPEERMQKGQSHLANLR
AQLANAKKP"

gene complement (398790..3989 /locus-tag="y0357"
54)
CDS complement (398790..3989 /locus-tag="y0357"
54)
    /note="residues 7 to 46 of 54 are
40.00 pct identical to residues
1819 to 1858 of 2565 from GenPept
: >gb|AAL12620.1| (AY051318)
Vitellin [Penaeus semisulcatus]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83947.1"
/db-xref="GI:21957042"
/translation="MLVGITHSISATLKTSLRMV
NQSRLNAWLTGNRLPVIIFTVTVA
AFRVNYGFSY"
gene complement (398957..4004 /locus-tag="y0358"
52)
    /note="gppA; disrupted by
frameshift"
/pseudo
gene complement (400456..4017 /gene="rhlB"
42)
    /locus-tag="y0359"
CDS complement (400456..4017 /gene="rhlB"
42)
    /locus-tag="y0359"
    /note="residues 1 to 428 of 428
are 88.78 pct identical to
residues 1 to 421 of 421 from E."

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coli K12 : B3780"
/codon-start=1
/transl-table=11
/product="putative ATP-dependent
RNA helicase"
/protein-id="AAM83948.1"
/db-xref="GI:21957043"
/translation="MSKTHLTERQKFSDFALHPLV
VEALENKGFQYCTPIQALALPLTL
SGRDVAGQAQTTGKTLAFLASTFHYLLSHPAEE
GROTNQPRALIMAPTRELAVQIHS
DAESELSSQVTGLKLGLAYGGDGYDKQLKVLESGVD
ILIGTTGRIDLHYAKONYINLGAIQ
VVVLDEADMYDLGIKDIRWLFRRMPSVDKRLN
MLFSATLSYRVRELAFEQMNNNAEY
VEVEPLQKTGHRIKEELFYPSNEEKMRLLQTLIE
EEWPDRCIIIFANTKHRCCEEIWGHIL
AADGHRVGLLTGDVAQKKRLRILEDFTKGLDIL
VATDVAARGLH1PLVTHFVNYYDLP
DDCEDYVHRIGRTGRAGESGHISLACEEYALNL
PAIETYTGHSIPVSKYNRSALLTD
LPAPKRLARTRTGNNGFRRNSAPRRSGAPRNNRKR
PG"

gene      401861..402187
gene="trxA"
/locus-tag="y0360"
gene="trxA"
/locus-tag="y0360"
/function="enzyme; biosynthesis of
cofactors, carriers: Thioredoxin,
glutaredoxin, glutathione"
/note="residues 1 to 108 of 108
are 87.03 pct identical to
residues 19 to 126 of 127 from E.
coli K12 : B3781; residues 1 to
108 of 108 are 87.03 pct identical
to residues 1 to 108 of 109 from
GenPept : >gb|AAC40210.1|
(AF044308) Escherichia coli
thioredoxin [Cloning vector
pBIOTRX-BirA]"
/codon-start=1
/transl-table=11
/product="thioredoxin 1"
/protein-id="AAM83949.1"
/db-xref="GI:21957044"
/translation="MSDKIIHLSDDSFDTDVLKA
SGLVLVDFWAECGPCKMIAPILD
EIAEYYEGRLTIAKLNIDDNQGTAPKYGIRGIFT
LLLFRDGEVATKVGALSKGQQLKA FLDANL"
/gene="rho"
/locus-tag="y0361"
/gene="rho"
/locus-tag="y0361"
/function="factor; RNA synthesis,
modification, DNA transcription"
/note="residues 1 to 419 of 419
are 95.22 pct identical to
residues 1 to 419 of 419 from E.
coli K12 : B3783"
/codon-start=1
/transl-table=11
/product="transcription"

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termination factor Rho; polarity suppressor"
/protein-id="AAM83950.1"
/db-xref="GI:21957045"
/translation="MNLTELKNTPVSDLITLGEN
MGLENLARMRKQDIIFSLKLQHAK
SGEDIFGDGVLIELQDGFGFLRSADSSYLAGPDD
IYVSPSQIRFNLRTGDTVAGKIR
PPKEGERYFALLKVNENVNYDKPENARNKILFENL
TPLHANSRLRMERGNGSTEDLTAR
VLDLASPIGRGQRGLIVAPPKAGKTMLLQNIATS
IAYNHPDCCVLMLLIDERFEEVITE
MQRLVKGEVIASTFDEPA\$RHVOVAEMIEKAKR
LVEHKKDVIILDSITRLARAYNT
VVPASGKVLTGGVDANALHRPKRFFGAARNVEEG
GSLTIIATATALVTGSKMDEVIEEE
FKGTGTMELHLSRKIAEKRVFFAIDFNRSGRTRKE
ELLTTTDELQKMWILRRILHPMGE
IDAMEFLISKLATAKTNDOQFDNMRRS"
/gene="rfe"
/locus-tag="y0362"
/gene="rfe"
/locus-tag="y0362"
/function="enzyme; central
intermediary metabolism:
Sugar-nucleotide biosynthesis,
conversions"
/note="synthesis of
enterobacterial common antigen
(ECA); residues 1 to 357 of 365
are 80.95 pct identical to
residues 1 to 357 of 367 from E.
coli K12 : B3784; residues 1 to
357 of 365 are 81.23 pct identical
to residues 1 to 357 of 367 from
GenPept :
>gb|AAG58979.1|AE005610-3
(AE005610)
UDP-GlcNAc:undecaprenylphosphate
GlcNAc-1-phosphate transferase;
synthesis of enterobacterial
common antigen (ECA) [Escherichia
coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="UDP-GlcNAc:undecaprenylp
hosphate GlcNAc-1-phosphate
transferase"
/protein-id="AAM83951.1"
/db-xref="GI:21957047"
/translation="MNLITMSTELIYIIFLFSMAF
LFVARKVAIKIGLVDPNKRKRHQ
GLIPLVGGISVFGVCF AFLITNQQIPHFRLYLA
CAGLLVFGCALDDRFDISVVKIRAF
VQALVGIGAMMAVAGLYLRSLGHAFGPWEMLGPF
GYVVTLFAVAIAINAFNMVDGIDG
LLGGLSCSVFSGAMGILLYQSGQMSLALWCFCAMIA
TIIPYILLNLGLLGRRYKVFMDGA
GSTLIGFTAIWILLQATOQGNAHPINPVTLWIIA
IPLDMIAIMYRRLRKGMSPFSPD
RQHIIHLIMRAGFTSRQAFVLITLAAALLAMIGV
IGERLTFIGEPEWVMLAFLLAFLLY

gene 405576..406655 GYCIKRAWRVARFIKRKFKRRMRASKNKHES"
CDS 405576..406655 /gene="wzzE"
/locus-tag="y0363"
/gene="wzzE"
/locus-tag="y0363"
/function="putative transport"
/note="residues 22 to 357 of 359
are 68.15 pct identical to
residues 15 to 349 of 349 from E.
coli K12 : B3785"
/codon-start=1
/transl-table=11
/product="putative transport
protein"
/protein-id="AAM83952.1"
/db-xref="GI:21957048"
/translation="MMKPESMSTDKTGSTNNEPS
VDNELDIRGLCRTLWRGKVWIIGM
AIIFAAIALGVSYLVKQWSATAITDKPTVNNLG
GYYSQQFLRNLIDRLRNLNSGLVSEQ
PGISDEAYGEFITQLAAZYDTRRDFWLQSDDYKQR
LEGDAKADAALLDELVNNNIVFTAR
DDKKIPNDISKLTAAETASDANKLLRGYIDFASQR
ASSHLNDEIQQAWAARTQSMKAQV
KRQEAVQAQVFDRVEAAVKQALKVAGQQGITSSQ
TDTPAEQQLADSKMFMGLGKPMLEAR
LETLLATGPSPFDIDYDQNQRAMLATLNVGPTLDDK
FQTYYRLRTPEDPVTRDSFRRVFL
LIMWGAIGALVGAGVVLRSSKAL"
gene 406882..408066 /gene="wecB"
CDS 406882..408066 /locus-tag="y0364"
/gene="wecB"
/locus-tag="y0364"
/function="enzyme; central
intermediary metabolism;
Sugar-nucleotide biosynthesis,
conversions"
/note="synthesis of
enterobacterial common antigen
(ECA); residues 15 to 394 of 394
are 78.15 pct identical to
residues 11 to 389 of 389 from E.
coli K12 : B3786; residues 15 to
394 of 394 are 78.42 pct identical
to residues 11 to 390 of 390 from
GenPept :
>gb|AAG58981.1|AE005610-5
(AE005610) UDP-N-acetyl
glucosamine -2-epimerase;
synthesis of enterobacterial
common antigen (ECA) [Escherichia
coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="UDP-N-acetyl glucosamine
-2-epimerase"
/protein-id="AAM83953.1"
/db-xref="GI:21957049"
/translation="MRPTCRHCLRLTDLKRTVK
VLTVFGTRPEAIKMALPVLHALAQD
DAFESRVCVTAQHREMLDQVRLRFEIQPPDYLDI
MRPGQQGLTEITCRILEGLKPVLEE

FKPDVILVHGDTTTLSASLAGFYHRIPVGHVEA
GLRTGDLSPWPEEANRQLTGHLA
MYHFAPTENSRQNLLREWPENRIFVTGNTVIDA
LFWVRDRVMNTPDRLRANLAQRYAF
LDTNKKMILVTGHRRESFGGGFERICSALAEIAR
KHPEVQVVPVHLNPNVSEPVNRI
LKGIDNIIILDPODYLPLFVLMNHAYLIITDSGG
IQEEAPSILGKPVLVMRDTERPEA
VDSGTLLLGVGTNINKIVDAVTRLLTDETAYHOMT
RAHNPGDGYACQRILKALKNHQV TL"
/gene="wecC"
/locus-tag="y0365"
/gene="wecC"
/locus-tag="y0365"
/function="enzyme; central
intermediary metabolism:
Sugar-nucleotide biosynthesis,
conversions"
/note="synthesis of
enterobacterial common antigen
(ECA); residues 1 to 420 of 420
are 82.14 pct identical to
residues 1 to 420 of 420 from E.
coli K12 : B3787; residues 1 to
420 of 420 are 83.57 pct identical
to residues 1 to 420 of 420 from
GenPept : >emb|CAD09395.1|
(AL627279) UDP-ManNac
dehydrogenase [Salmonella enterica
subsp. enterica serovar Typhi]"
/codon-start=1
/transl-table=11
/product="UDP-N-acetyl-D-mannosami
nuronic acid dehydrogenase"
/protein-id="AAM83954.1"
/db-xref="GI:21957050"
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AFASRKKVIGDVNAHAVETINR
GAIHIVEPDLDKVKIAVEGGYQLQAVTKPQAADA
FLIAVPTPFKGDHEDPMIFVESAA
KSIAFPVLKKGDVLILESTSPTVGATEQMAQWLAE
RPDLSPFPQQAGEAADINIAYCPER
VLPGQVMVELIQNDRVIGGMTPKCSARASALYKI
FLEGECCVTSNRTAEMCKLTENSF
RDVNIIAFANELSLICDEQGINWELIRLANRHPR
VNILQPQPGVGGHCAIVDPWFIVS
QNPQLPQAVLHHTARLNVNDGKPLWVVDVRKAADVDC
LAASDKRASEVKIAFCFGFLAFKPDI
DDLRESPAVGVARLIAEWHVGETLVVPEPNVEQLP
KSLMGLVTLKDOTALQQADVLVM
LVDHKQFKAIKPEDIKQQWIVDTKGVWR"
/gene="rffG"
/locus-tag="y0366"
/gene="rffG"
/locus-tag="y0366"
/function="enzyme; central
intermediary metabolism:
Sugar-nucleotide biosynthesis,
conversions"
/note="residues 3 to 355 of 357
are 82.15 pct identical to
residues 1 to 353 of 355 from E.

coli K12 : B3788; residues 1 to 357 of 357 are 85.43 pct identical to residues 1 to 357 of 357 from GenPept : >gb|AAC12869.1| (AF044332)
 dTDP-D-glucose-4,6-dehydratase;
 RffG [*Pectobacterium carotovorum* subsp. *atrosepticum*]
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 /transl-table=11
 /product="dTDP-glucose 4,6-dehydratase"
 /protein-id="AAM83955.1"
 /db-xref="GI:21957051"
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 VVMHLAAESHVDRSIDGPAAFIET
 NVVGTYTLLAEARHYWQQLSVEAKQAFRFHHIST
 DEVYGDHLGTDDLFTETTPYAPSS
 PYASAKASSDHVRAWLRTYGLTTLVTCNSNNYG
 PYHFFPEKLIPLVILNALAGKPLPV
 YGNGAQVRDWLYVEDHARALYQVVTTEGVVGETYN
 IGGHNERKNIEVVETICALDELV
 PAKPAGIAHYRDLITYVKDRPGHDMDRYAIDAGKI
 ERELGWRPQETFESGIRKTVLWYL
 NNESWRRVQDGSYAGERRLGLSD"
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 /locus-tag="y0367"
 /gene="rffH"
 /locus-tag="y0367"
 /function="enzyme; central intermediary metabolism:
 Sugar-nucleotide biosynthesis, conversions"
 /note="residues 71 to 363 of 363 are 86.68 pct identical to residues 1 to 293 of 293 from E. coli K12 : B3789"
 /codon-start=1
 /transl-table=11
 /product="glucose-1-phosphate thymidylyltransferase"
 /protein-id="AAM83956.1"
 /db-xref="GI:21957052"
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 LCLMVSGDGMYQEIVCIRRHLHVSGERMKGIILAG
 GSGSRLHPITRGVSKQLLPIYDKP
 MIYYPLSVLMLAGIRDVLIISTPEDLPSFQRLLG
 NGDEFGINLSYAAQPSPDGLAQAF
 IIGEAFIDNEPCCLVLGDNIFYFGQGFSPKLAVA
 ARQQGATVFGYQVMDPERFGVVVEF
 DDNFRLSIEEKPSQPKSNWAVTGLYFYDNQVVD
 FAKQVKPSARGELEITSINQMYLD
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 EKRGQFKIACLEELIAWRNGWLDDD
 GVKAATATALAKTGYGKYLLDLHARPRQY"
 /gene="wecD"
 /locus-tag="y0368"
 /gene="wecD"
 /locus-tag="y0368"

/note="residues 63 to 263 of 264
are 49.25 pct identical to
residues 1 to 181 of 181 from E.
coli K12 : B3790"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83957.1"
/db-xref="GI:21957053"
/translation="MRQPWRKPVMANICWIYMFV
HASIEPLGWSEEFFQRQSAKLFSDSAPPNPAELAAFTLVOAKVPTHRLLDLIDAL
SQLDFHLVEGEIDLSSLVGEKEGI
GTENATSEPNMGAYSLRVATEADIPQLRRAASA
FALSRFRAPWYDAQDSGRFYALWVEKA
VLGTFDHQCLLVLDPDQPVGFVTLRDLQDG
SARIGLLAVPGQAQSFKIGLRLMS
AAKWCQHHGLHRLRVATQMSNIAALRLYIRSGA
SIESTAYWLRCG"
gene 412207..413412 /gene="wecE"
CDS 412207..413412 /locus-tag="y0369"
/gene="wecE"
/locus-tag="y0369"
/function="putative regulator"
/note="residues 26 to 400 of 401
are 84.79 pct identical to
residues 1 to 375 of 376 from E.
coli K12 : B3791"
/codon-start=1
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/product="putative regulator"
/protein-id="AAM83958.1"
/db-xref="GI:21957054"
/translation="MLLYVSIFVVVPPPLRVPRIG
YAGDEMIFPNTPIVGTELGYMOA
AMSSGKLCGCGGFTRCQOWMEKRFRNCPKVLLTP
SCTASLEMAALLLDIKPGDEVIMP
SFTFVSTANAFVLRGAKMVFVDIRPDTMNIDET
IEAAITDKTRIVLPVHYAGVACEM
DTIMALAKHNLFVVVEDAAQGVMTYKGKALGTI
GHIGCFSPHETKNYTAGGEKGATL
INDESLIDRAEIIREKGTNRSQFFRGQVDKYTWR
DIGSSYLMSDLQAAYLWGQLEAAE
QINERRLALWHGYYNAFKPLADAGRIDLDPVIPGN
VVQNAHMPYIKLRDIEERSAFISY
LKEADIMAVFHYIPLHACPAGEAFGRMAGEDRFT
SKESERVLRLPIFYNLTDVNQSTV
INTVLSFFF"
gene 413414..414670 /gene="wzxE"
CDS 413414..414670 /locus-tag="y0370"
/gene="wzxE"
/locus-tag="y0370"
/function="putative carrier"
/note="residues 1 to 416 of 418
are 75.00 pct identical to
residues 1 to 416 of 416 from E.
coli K12 : B3792; residues 1 to
416 of 418 are 75.00 pct identical
to residues 1 to 416 of 416 from
GenPept : >emb|CAD09390.1|
(AL627279) putative
lipopolysaccharide biosynthesis

| | | |
|------|----------------|--|
| | | protein [Salmonella enterica
subsp. enterica serovar Typhi]
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/transl-table=11
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/protein-id="AAM83959.1"
/db-xref="GI:21957055"
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GLLVVKLLAVTFPGPSVGQAGNFR
QLIIVLGVLSGAGIFNGITKYVAEYHQPPERLRA
MLGTSSTIVLGFSTLLALVFLLAA
KPVSIALEFGHADYQNVVRRAIFIOMGIAVGNLFL
AILKGYRDAKGNALAIIIGGSILGV
VAYYICFOIGGYSGALVGLGLPALVVLPAAML
YRRRTIPLRLKPHWDKALASHLG
KFTLMALITSVTLPVAYVMMRHLANNYQWDAVG
IWQQVSSISDAYLQFITAFTVYL
LPTLSRLDKGAISREIFRSLKFVLPAVAASLT
VWLLRDFAIWLLFSHQFTAMRDLF
AWQLVGDVLKVGSYYFPGYLVIAKASLRFYILAEV
SQFLLLTGFAYWLIPMNGSLGAQ
AYMATIYIVYFALCSCAFLVYRRHSAP" |
| gene | 414693..415778 | /gene="wecF"
/locus-tag="y03'1"
/gene="wecF"
/locus-tag="y03'1"
/function="enzyme; central
intermediary metabolism;
Sugar-nucleotide biosynthesis,
conversions"
/note="synthesis of
enterobacterial common antigen
(ECA); similar to B3793 in E. coli
K-12; residues 1 to 359 of 361 are
64.90 pct identical to residues 1
to 357 of 359 from GenPept :
>emb CAD09389.1 (AL627279)
conserved hypothetical protein
[Salmonella enterica subsp.
enterica serovar Typhi]"
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Fuc4NAc transferase"
/protein-id="AAM83960.1"
/db-xref="GI:21957056"
/translation="MITLTHVLGSDIPHNNLTVL
RFFNDVLAKEPCLPVEQVRHEFMVAAK
ETAFSSFPQLINTYSDDKKAAEAVIARAQADR
SARFFWHQGFVNTLWLAALLSGKIK
PGQVYWHVWGADLYEDAKSLKFRLFYLLRRIAQG
RVGHFATRGDLIHQYQRHIFPRVPA
SLLYFPTRMDPALTAINIDKPLAGPMTILVGNSG
DTTNRHIEALKAIHQQFGPDVRVI
IPMGYPANNEAYIEQVRQAGLAGFSQDNLRLITE
QIPFDYDLNIRECDCDLYGIFTNRQ
QGIGTLCLLTQFGVFPVLSRKNPFWQDQLAEQHIP
VFFYGDTLDEPMIREAQRLAGLD
KQAIASFNPNYIEGWKQALALAAGEHP" |
| CDS | 414693..415778 | |
| gene | 415775..417139 | /gene="wecF"
/locus-tag="y03'2"
/gene="wecF" |
| CDS | 415775..417139 | |

/locus-tag="y0372"
/function="enzyme; central
intermediary metabolism:
Sugar-nucleotide biosynthesis,
conversions"
/note="synthesis of
enterobacterial common antigen
(ECA); residues 1 to 444 of 454
are 77.97 pct identical to
residues 1 to 445 of 450 from E.
coli K12 : B3793; residues 1 to
444 of 454 are 77.97 pct identical
to residues 1 to 445 of 450 from
GenPept :
>gb|AAG58989.1|AE005610-13
(AE005610) TDP-Fuc4NAc:lipidII
transferase; synthesis of
enterobacterial common antigen
(ECA) [Escherichia coli O157:H7
EDL933]"
/codon-start=1
/transl-table=11
/product="TDP-Fuc4NAc:lipidII
transferase"
/protein-id="AAM83961.1"
/db-xref="GI:21957057"
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LTFYFGPLTCMLVFQFGVAVVPVEYLLYAMLSA
TAFYGIYVVTYKTRLRQPRSQPT
PIFTMNRVETNLTVLLALVAVGTVGIFFMQNGF
LLFKLDSSYSKIFSSDVSGVALKRF
FYFFFIPAMLVVYFLKQDRRAWFFFLASTVAFGIL
TYVIVGGTRANIIIAFSLELFIGI
VRGWITLVMLAAGVFGIVGMFWLALKRYGLDVN
GAEAFYTFLYLTDITFSPWENLGL
LLQNYDKIDFQGLAPIVRDFYVFIPSALWPERPD
LVLNTANYFTWDVLNDHSGLAISP
TLIGSLVMGVLFIPGLGAIIVVGLIIKWFDWLYE
QGKAESNRYKAIALQSFCFGAVFN
IIVLAREGLDSFVSRRVFFCIVFGACLVLAKLLY
WLFDTAGLIKRGQIKSNRLSTPNA GNQL"
/gene="wecG"
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/function="enzyme; central
intermediary metabolism:
Sugar-nucleotide biosynthesis,
conversions"
/note="synthesis of
enterobacterial common antigen
(ECA); residues 1 to 246 of 246
are 70.73 pct identical to
residues 1 to 246 of 246 from E.
coli K12 : B3794"
/codon-start=1
/transl-table=11
/product="probable
UDP-N-acetyl-D-mannosaminuronic
acid transferase"
/protein-id="AAM83962.1"

gene 417148..417888
CDS 417148..417888

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IRRKYQPQELSRSVAGADLNEALMQ
RAGQQGTPVFLVGKPDVLAETEAKLRAQWNVN
VGSQDGTYTPEQREALFARIAASG
AAIVTVAMGSPQEIMFRDCRKYPDALYMGVGG
TYDVFSTSHVKRAPKIQWNNQGLEWL
YRLLAQPSRIRQLKKFVGYYYSGRL"
gene complement(418178..4182 /locus-tag="y0374"
61)
CDS complement(418178..4182 /locus-tag="y0374"
61)
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83963.1"
/db-xref="GI:21957060"
/translation="MNEGLTAPRGTPVAYATTT
TARFFFN"
/locus-tag="y0375"
/locus-tag="y0375"
/function="putative transport"
/note="residues 1 to 454 of 463
are 79.73 pct identical to
residues 1 to 452 of 461 from E.
coli K12 : B3795; residues 1 to
454 of 463 are 80.39 pct identical
to residues 1 to 452 of 461 from
GenPept :
>gb|AAG58991.1|AE005611-1
(AE005611) putative amino
acid/amine transport protein
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="putative amino
acid/amine symporter"
/protein-id="AAM83964.1"
/db-xref="GI:21957061"
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LIALGGTIGVGLFMGSASTLKWAQ
PSVLLAYIIAGLFVFFIMRAMGEMLYLEPVAGSF
AVYAHKYLSPYFGYLTAWGYWFMW
IAVGISEITAIGVYVQFWFPEIPQWLPAIAGVAI
VALANLAALKVLYGELEFWFWMAMIKV
TTIIVMILVGLGVIFFGFGGNHQPIGFDNLTAHG
GFFAGGWKGFLFALCIVVASYQGV
ELVGITAGEARNPQVTLRRAINNIlWRILIFYVG
AIFVIVTIPWNGIGTEGSFVLT
FAKIGIVAAAGIINFVILTAALSGCNSGMSGGR
MLYALAKNRQLPAGLTKLSASGVF
VYCIAITILCLLVGSSLNYIIPNPQQFVIVYSA
SVLPGMVPWFVVLVCQLRFQVHK
AALQOHPFKSILFPYVNLTIAFLICVLVGMGIN
PDTRLSLLVGAIFLALVTGCFYFV
GMHKPKAMEAERL"
/locus-tag="yt006"
/locus-tag="yt006"
/product="tRNA-Arg"
/note="anticodon: CCG"
gene tRNA 419952..420025
419952..420025

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gene 420112..420184 /locus-tag="yt007"
tRNA 420112..420184 /locus-tag="yt007"
/product="tRNA-His"
/note="anticodon: GTG"
gene 420204..420287 /locus-tag="yt008"
tRNA 420204..420287 /locus-tag="yt008"
/product="tRNA-Leu"
/note="anticodon: CAG"
gene complement(420253..4207
41) /locus-tag="y0376"
CDS complement(420253..4207
41) /codon-start=1
/transl-table=11
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/protein-id="AAM83965.1"
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CDQRELIMEVINKVVPARRIRRIKGKKLQVGLSV
WQNRIIIIFRKTPHCVGVSSEIGR
RERIRTSDFPLVFNQLRYQAALLADFLLLTLHGLS
TYVHVNIKYLHVCVVRREGLEPS RP"
gene 420366..420439 /locus-tag="yt009"
tRNA 420366..420439 /locus-tag="yt009"
/product="tRNA-Pro"
/note="anticodon: TGG"
repeat-region 421164..421873 /note="insertion element"
/insertion-seq="IS1541a"
/locus-tag="y0377"
/locus-tag="y0377"
/function="IS and transposon
related functions"
/note="IS1541a; residues 1 to 169
of 169 are 100.00 pct identical to
residues 1 to 169 of 169 from
GenPept : >gb|AAC82673.1|
(AF074611) transposase [Yersinia
pestis]"
/codon-start=1
/transl-table=11
/product="putative transposase"
/protein-id="AAM83966.1"
/db-xref="GI:21957063"
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EKSLAHTRNCKYHIVFAFKYRRQ
VFYREKRRRAIGSILRKLCEWKNVNILEAEYCVDH
IHMLLEIPPKMSVSGFMGYLKKGKS
SLMLYEQFGDLKEFKYRNREFWCGRGYYVDTVGKNT
ARIQEYIKHQLEEDKMGEQLSIPIY
PGSPTGKR"
gene complement(421960..4231 /gene="hemY"
80) /locus-tag="y0378"
CDS complement(421960..4231 /gene="hemY"
80) /locus-tag="y0378"
/function="enzyme; biosynthesis of
cofactors, carriers: Heme,
porphyrin"
/note="a late step of protoheme IX
synthesis; residues 1 to 395 of

406 are 70.63 pct identical to
 residues 1 to 395 of 398 from E.
 coli K12 : B3802"
 /codon-start=1
 /transl-table=11
 /product="hemY protein"
 /protein-id="AAM83967.1"
 /db-xref="GI:21957064"
 /translation="MLRVLLLFLVLTVGIVLGPMLAGHOGYVLIQTDNYNVITSVTGLAIMLVLLVAFFFIVEWLRRIFRTGARTRGWFLGRKRTRARNQMKAAALIKLAEGDFLQVEKLLTRNADHAEQPMVNLYLAAEAAQQRGDEFRTNQYLERAAEVADGDQLPVNITRVRQIQLAQGHIAARHGVDRLLDQAPRHPFEVRLAEQAYLRSGAYRSLLDILPAMSKTQIHTPEEEVAALEQQAYIGIMNCMADEGSEGGLKRWWKDQSRSKVRNEIPLQVALAEHLIECDDHDVAQKIIILDSLKHQYDERLALLIPRLKAGNPPELEKSLRQIQQHGTAPLNSTGQLMLKHGEWEKASEAFKAALAQRPDGYDYAWLADALDKLHRPEDAAQARREGLLLTLRONGESSALTKLH"

| | | |
|------|--------------------------|--|
| gene | complement (423183..4243 | /gene="hemX" |
| | 16) | /locus-tag="y0379" |
| CDS | complement (423183..4243 | /gene="hemX" |
| | 16) | /locus-tag="y0379"
/function="enzyme; biosynthesis of cofactors, carriers: Heme, porphyrin" |

<-----User Break----->

145 of 145 are 46.15 pct identical
 to residues 1 to 126 of 127 from
 GenPept : >gb|AAL22425.1|
 (AE008864) putative
 acetyltransferase [Salmonella typhimurium LT2]"
 /codon-start=1
 /transl-table=11
 /product="hypothetical protein"
 /protein-id="AAM84010.1"
 /db-xref="GI:21957111"
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 AWQQWITEQGRPLFAARFNERLLGAVKVAVYDQQA
 ELQDLCVREVTRRRGVGVLIEET
 LRQLPEIKHWYLNGGDLTAAERPQMNSFMLACGFSHEAQGWRR"

| | | |
|------|----------------|---|
| gene | 470375..471505 | /gene="livK" |
| | 470375..471505 | /locus-tag="y0422" |
| CDS | 470375..471505 | /gene="livK"
/locus-tag="y0422"
/function="transport; transport of small molecules; amino acids, amines"
/note="residues 12 to 376 of 376 are 75.34 pct identical to residues 6 to 369 of 369 from E. coli K12 : B3458; residues 12 to 376 of 376 are 75.61 pct identical" |

to residues 6 to 369 of 369 from
GenPept :
>gb|AAG58565.1|AE005569-5
(AE005569) high-affinity
leucine-specific transport system;
periplasmic binding protein
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="high-affinity
leucine-specific leucine-specific-b
inding periplasmic protein of
high-affinity branched-chain amino
acid ABC transporter transport
system; periplasmic binding
protein"
/protein-id="AAM84011.1"
/db-xref="GI:21957112"
/translation="MGNNSRMKLTGKVLLAGCMA
MAMSHSVLAQD1KVAIVGAMSGPV
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DDACDPKQAVAVANKVINDGIRYV
IGHLCSSSTQPASDIYEDEGVIMITPAATNADLT
TRGYKMINRTTGLDSDQGFTAAKY
IVETIKPKRIA VVHDKQQYGEGLARSVRDSLKEQ
GAEVVLFEGVTAGDKDFSTLVARL
KKENVDVFVFGGYYPEMGOILRQAKQAGLTARFM
GPEGVGNSSSLNIAGEASEGMLVT
LPKRYDQVPANQPIVDALKAKKLDPTGPFWTTY
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LKTGKPVETVMGPLSWDDKGDLKGFEFGIFEWHA
DGSSTAVE"
/gene="livH"
/locus-tag="y0423"
/gene="livH"
/locus-tag="y0423"
/function="transport; transport of
small molecules; amino acids,
amines"
/note="residues 1 to 308 of 308
are 87.33 pct identical to
residues 1 to 308 of 308 from E.
coli K12 : B3457; residues 1 to
308 of 308 are 87.66 pct identical
to residues 1 to 308 of 308 from
GenPept : >gb|AAL22423.1|
(AE008864) ABC superfamily
(membrane), branched-chain amino
acid transporter, high-affinity
[Salmonella typhimurium LT2]"
/codon-start=1
/transl-table=11
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branched-chain amino acid ABC
transport system membrane
permease"
/protein-id="AAM84012.1"
/db-xref="GI:21957114"
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TYALIAIGYTMYGIIGMINFAGH
EVYMISSYVSFIVIAALMMVGIDASWLLIGCAFL
VSIVIASTYGVSIERVAYKPVRRS

KRLIALISAIGMSIFLQNYVSLTQGSRDLALPSL
VTGWTILGESNGFAATISTMQLTI
WIVTFLAMLALTFLFIRYSRMGRACRAEADLKMA
SLLGINTDRVISLTFLVIGALMAAV
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SIPGAMIGGLVLGVVAEALTSAYLS
TEYKDAVSFALLIVVLLVMPTGILGRPEVEKV"
/gene="livM"
/locus-tag="y0424"
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/locus-tag="y0424"
/function="transport; transport of
small molecules; amino acids,
amines"
/note="residues 1 to 428 of 428
are 79.43 pct identical to
residues 1 to 425 of 425 from E.
coli K12 : B3456"
/codon-start=1
/transl-table=11
/product="inner membrane permease
of high-affinity branched-chain
amino acid ABC transport system"
/protein-id="AAM84013.1"
/db-xref="GI:21957115"
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SFVMSGQLQLDGTTRLVVOQASEVR
WLWIGAGCLVVFCFCQLVRLPIQQGIKKVSGPAWV
LPSFDGTTPRQKLLAAVIIAAVA
WFPLVSRGSVDIATLTLIXVMLGLGLNVVVGLSG
LLVLGYGGFYIAIGAYTYALLNNHY
GLGFWESELPLAGITAALSGFLLGFVPLRLRGDYL
AIVTLGFGEIVRILLNNTEITGG
PNGISQIKPFLFGLEFSRTAKDGGWDTFHNFHG
LTYDPSHRIIFLYVALLLLVIITL
FVINRLLRMPLGRANEALREDEIACRSLGLSPTK
IKLTAFTISAAFAGFAGTFLFAARQ
GFVSPESFTFVESAFVLAIVVLGGGMGSQFAVILA
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QA"
/gene="livG"
/locus-tag="y0425"
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/function="transport; transport of
small molecules; amino acids,
amines"
/note="residues 4 to 255 of 255
are 82.14 pct identical to
residues 3 to 254 of 255 from E.
coli K12 : B3455; residues 4 to
255 of 255 are 83.33 pct identical
to residues 3 to 254 of 255 from
GenPept : >gb|AAL22421.1|
(AE008864) ABC superfamily
(atp-bind), branched-chain amino
acid transporter, high-affinity
(Salmonella typhimurium LT2)"
/codon-start=1
/transl-table=11
/product="ATP-binding component of

high-affinity branched-chain amino acid ABC transport system"
 /protein-id="AAM84014.1"
 /db-xref="GI:21957116"
 /translation="MNGQPLLTVEGLSMSMRFGGLL
 AVNNVGLTLNQEIVSLIGPNGAG
 KTTIFNCLTGFYRPTGTTKLRERHLEGLPGQMI
 ARMGVIRTFQHVRLFREMVTIENL
 LVAQHQHLKSGIFAGLLKTFGFRRAEADALARAA
 TWLERVGLLALANRQAGNLAYGQQ
 RRLEIARCMVTRPELLMDEPAAGLNPKETDELN
 QLIMELRDQHQVSLLIEHDMKLV
 MGISDRIYVVNQGTPLAQQLPAEIRNNPDVIRAY
 LGE"
 gene 474674..475405 /gene="livF"
 CDS 474674..475405 /locus-tag="y0426"
 /gene="livF"
 /locus-tag="y0426"
 /function="transport; transport of small molecules; amino acids, amines"
 /note="residues 11 to 243 of 243 are 87.12 pct identical to residues 9 to 241 of 241 from E. coli K12 : B3454"
 /codon-start=1
 /transl-table=11
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 /protein-id="AAM84015.1"
 /db-xref="GI:21957117"
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 MREIAIAIVPEGRRVFSRMT
 VEENLAMGGFFADRQQYQORIERYVDLFPRFLFER
 RIQRAGTMSGGEQQMLAIGRALMS
 QPKLQLLDEPSLGLAPIIIILQIFDTIQQLREEGMTIFLVEQNANQALKLADRGYVLEN
 GRIVELDTGAALLANEAVRSAYLGG"
 gene 475633..476094 /locus-tag="y0427"
 CDS 475633..476094 /locus-tag="y0427"
 /note="residues 26 to 113 of 153 are 28.40 pct identical to residues 181 to 264 of 413 from GenPept : >gb|AAC44570.1| (U61140) ORF1 [Mycoplasma mycoides subsp. mycoides SC]"
 /codon-start=1
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 /protein-id="AAM84016.1"
 /db-xref="GI:21957118"
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 NLSLNRRNIYLDTSDADRECRIPQTQLSPDQNVDSG
 TKKPFWISKYLCITTLY"
 gene complement (476209..4773 /locus-tag="y0428"
 CDS 15) complement (476209..4773 /locus-tag="y0428"

15)

/note="residues 16 to 44 of 368
are 51.61 pct identical to
residues 242 to 272 of 621 from
GenPept : >gb|AAF48396.1|
(AE003497) CG9521 gene product
(Drosophila melanogaster)"
/codon-start=1
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TLEDNSVAVSFDVTLVADLFETDRGPHLQRWKK
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DGSADFISRPGDIQNMMSLNGIPVQEIDYNLQEAR
FVSTHAFSNQSYHVSFNITANALK
HIRMGATIGGVHLSEGVSYSVRSPPQGVAFNQSGN
QCEFDDPTEIAFSPHALYIEPKFR
LGSAIWQLKSLLDLHLLDSTAQNHHGLAPLVNGP
ANRFCIHYPAIGTQNFRYRMYISASN
LNGLAESSRYFQLKDQNQGEHIINYKVTLKNHEDS
EADFSLPKEKKFIQLKSDTSSGG
AQMCWSPRIVYSTDITDKGHYTDTLNFTITPLA
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gene complement(477393..4779 /locus-tag="y0429"
11)
complement(477393..4779 /locus-tag="y0429"
11)
/note="residues 61 to 118 of 172
are 29.31 pct identical to
residues 781 to 838 of 987 from
GenPept : >dbj|BAB75624.1|
(AP003594) ORF-ID:alr3925
hypothetical protein [Nostoc sp.
PCC 7120]"
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/protein-id="AAM84018.1"
/db-xref="GI:21957120"
/translation="MNTIKMAITLLLLSWHTCWA
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HGGYWDN1KLHNSPENHAVYEVEVPVAVKLRRQE
GYQISIKNPLILTRQSDFASIAEQ
TFSPAEVWRGNNRTNLRLLSAVPESFSVPPQATR
HTTDYVLQWISAKAPAGDNTAGKY
HGQLTTLVEFVNS"

gene complement(477973..4786 /locus-tag="y0430"
35)
complement(477973..4786 /locus-tag="y0430"
35)
/note="residues 6 to 174 of 220
are 27.27 pct identical to
residues 1 to 173 of 238 from
GenPept : >emb|CA87760.1|
(Z47800) CotB [Escherichia coli]"
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/protein-id="AAM84019.1"

/db-xref="GI:21957121"
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 QQPLLFATPLKLTLGPRQSGKIFL
 HALGAPEQEQVYRLLAVVPSNHLKISGNNTAVGV
 QISYMGHLRHPASIQHQWTHRCI
 AGKPELHNTGNTRLYWHQLQAQGOMIDDFTLYPG
 RYRQLAFNELQGKVEDQQAQNVLQCP SG"
 gene complement (478592..4793 /locus-tag="y0431"
 11)
 CDS complement (478592..4793 /locus-tag="y0431"
 11)
 /note="residues 11 to 221 of 239
 are 21.02 pct identical to
 residues 3 to 206 of 236 from
 GenPept : >emb|CAD08770.1|
 (AL627266) putative fimbrial
 protein [Salmonella enterica
 subsp. enterica serovar Typhi]"
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 /translation="MFPRLLIPITGFMKYLYSILS
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 EAQELKRTVQVNVNSGDTPLYLDDITLQRVDNPVGVN
 PERKTPISEISQPEMIFNPNRITL
 GPRQKRDTLIPLKSPVQETLYRLYINPVLNIKA
 VGDGEDKSKVHAPMTISIGYVGLI
 HHLPAAQCTRHWQHOCSTTGELETLTATGTVHSK
 FKQLESGGNAALADSNLNYPGTAL
 TLPVQLQNGEVDFGEKFSLRCH"
 gene complement (479296..4816 /locus-tag="y0432"
 44)
 CDS complement (479296..4816 /locus-tag="y0432"
 44)
 /note="residues 53 to 775 of 782
 are 20.33 pct identical to
 residues 49 to 830 of 869 from
 GenPept : >gb|AAC41416.1| (M55661)
 colonization factor antigen c
 [Escherichia coli]"
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 AAEEENNLSQLLGVLDSTSITLSPITFSEEEQQLQF
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 IPYLOCKTGCDYTLGCHRVALDKVNNTLTITNNN
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 NTLQSONTTPMSOSTYOPVNRPOYO
 RLTQKGIGSWYLQKNFSALYLRTRQNNLDDNNAG
 SVHTLINFALDQFVTLGSQSYLAI
 DKPSTGSIVLYAAQDGDEIYRDNQLIRRIPAQI
 GRNEIDYSQLPGGGYYNVEIRLVDR
 LGRIVSQENQTISNIGNQTNNGWFLTMGKGPAKG

KKTPLVQFGRSRVIESVQTNTL
 LKDDAHWAVEANVSRPLSLNKVNTPTGGLMSG
 EKRSGGYVRLNGNNNTLGYFSLAR
 YQSPYVSRYPDGSSTGSYTRRIGPTQLSYQFN
 QYRNRRQHRIQSQWDWQLQFNL
 LSLGLQNQGQWNSHNNYGVFLNTLSFGQSASI
 NTAYTQQLNTSASYQKEFDNYC
 ASTLGVSASGKLNNSVGGFAKRSRGDISGRV
 GIDNQITNGGISYNGMLALSSQGV
 ALGRSSYSGAALLIKAPALGGTPYSFHVEDSPIT
 GGGTYAIIPVPRYQDRFFFRTHTDR
 SDMDMNQIQLPVNIVRAHPGQVFSGEADITLNLLY
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gene complement(481896..4823 /locus-tag="y0433"
 87)
 CDS complement(481896..4823 /locus-tag="y0433"
 87)
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 colonization factor antigen b
 [Escherichia coli]"
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 organic acids, alcohols"
 /note="sn-glycerol 3-phosphate ABC
 transport system; residues 6 to
 439 of 439 are 80.18 pct identical
 to residues 4 to 437 of 438 from
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 439 of 439 are 82.06 pct identical
 to residues 3 to 437 of 438 from
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 (peri-perm), sn-glycerol
 3-phosphate transport protein
 [Salmonella typhimurium LT2]"
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 RLLSQPFNSSTPVLYNNKEAFKKA
 GLDPEQQPKTWQELAADTAKLRAAGSSCCGYASGW
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 DGTDAVLEFNKPQLQVKHIIQLSDMNKKGDFTYFG
 RKDESTSKFYNGDCAITTASSGSL
 ASIRHYAEKFNFVGGMMPYDADAKNAPQNAIIGGA
 SLWVMDGDKDKEYKGVAEFLQYLV
 KPEIAAEWHQKTYGLPITTAAYELTKQQGFYEQN
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 /function="transport; transport of
 small molecules; carbohydrates,
 organic acids, alcohols"
 /note="sn-glycerol 3-phosphate ABC
 transport system; residues 1 to
 295 of 295 are 79.32 pct identical
 to residues 1 to 295 of 295 from
 E. coli K12 : B3452; residues 1 to
 295 of 295 are 80.33 pct identical
 to residues 1 to 295 of 295 from
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 (membrane), sn-glycerol
 3-phosphate transport protein
 [Salmonella typhimurium LT2]"
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 protein, permease"
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 GSRLYQTLLILPYAVAPAVAALWIFLFDPLGL
 ITHALAKLGYSWNHAQNSQAMFL
 VVLASVWKQISYNFLFELAALQSIPKSLVEAAAI
 DGAGFVRRFFNLVLPFLISPVSFFL
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 gene 485443..486288
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 /gene="ugpE"
 /locus-tag="y0436"
 /function="transport; transport of
 small molecules; carbohydrates,
 organic acids, alcohols"
 /note="sn-glycerol 3-phosphate ABC
 transport system; residues 1 to
 281 of 281 are 77.58 pct identical
 to residues 1 to 281 of 281 from

E. coli K12 : B3451; residues 1 to 281 of 281 are 79.71 pct identical to residues 1 to 281 of 281 from GenPept : >gb|AAL22415.1| (AE008864) ABC superfamily (membrane),sn-glycerol 3-phosphate transport protein [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="inner membrane permease" /protein-id="AAM84025.1" /db-xref="GI:21957128" /translation="MIEENRRGLDIFCHIMLIIGV LLILFPFLYVAFVAAASLDDSQVFQA PMTLIPGPHLWNQNIISHIWHAGVGNNSTPFGMLL NSFVMAFAITVGKIKITVSIISAYAI VYFRFPLRNLFWFYLIFTLMLPVEVRIFTIEVI ANLNLLDSYTGLTLPLMASATATF LFRQFFMTLPDELLEARIDGAGAMRFFWDIVLP LSKTNLAALFWITFIIYGWNQYLPW ILITSDASTMGTAVAGIRSMISTSGAPTOQNQVM AMLTLLPPVVVLLMQRWFVRGL VDSEK"

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| gene | 486295..487368 | |
| CDS | 486295..487368 | |
| gene | 487365..488114 | |

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CDS 487365..488114

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multipurpose conversions"
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are 72.95 pct identical to
residues 3 to 245 of 247 from E.
coli K12 : B3449; residues 4 to
247 of 249 are 73.77 pct identical
to residues 3 to 245 of 247 from
GenPept :
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(AE005568) glycerophosphodiester
phosphodiesterase, cytosolic
[Escherichia coli O157:H7 EDL933]"
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glycerophosphodiester
phosphodiesterase"
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QLDAGDWFSKAFRGERPLLSEVA
ARCAQHGMANIEIKEPTTGTDAPTGRAIALAARA
LWQGQPPIPPLLSSFSVDAALAAAQL
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gene 488215
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4 FILE USPAT2
0* FILE WATER
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2008

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L3 13 DUP REM L2 (4 DUPLICATES REMOVED)

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